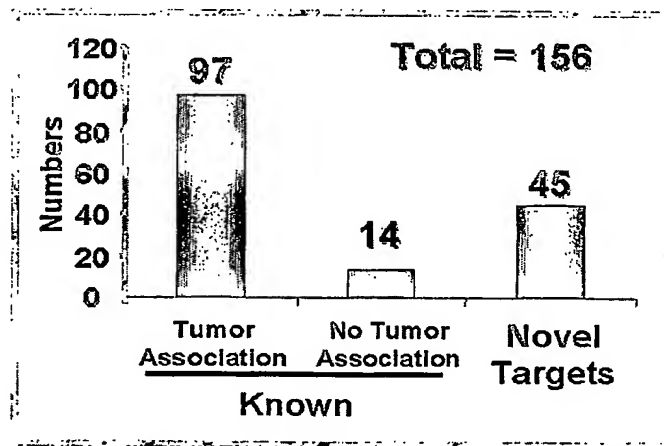5   Figure 1. Advantage of Efficacy-First Discovery™ Method

10

Figure 2. Highly Enriched Tumor Targets

siRNA-Mediated Target Validation
(MDA-MB-435 Xenograft Model)

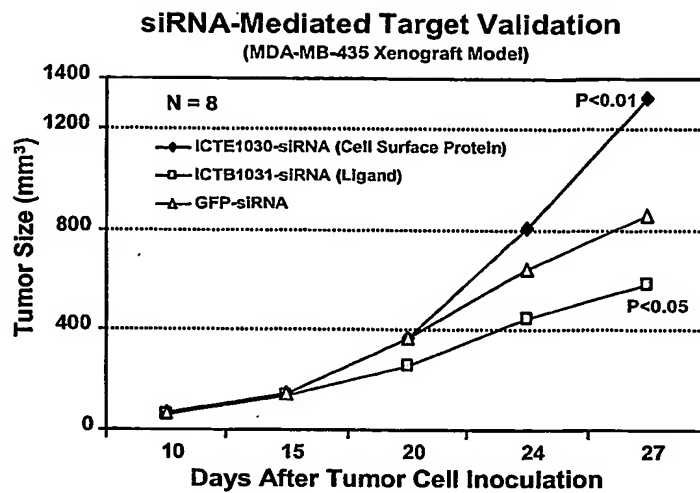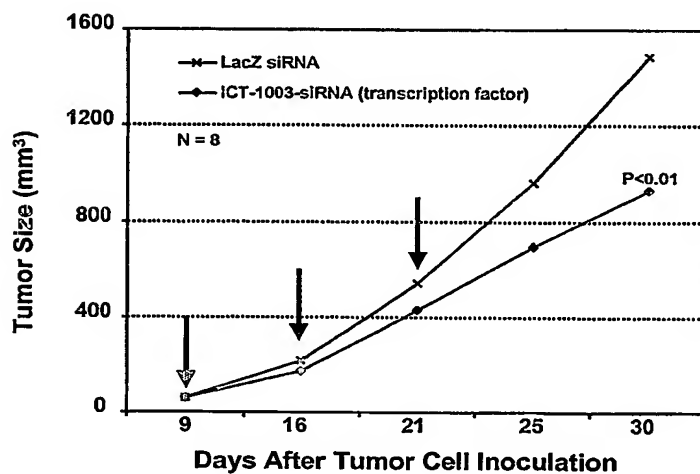Figure 3. Two Novel Targets Were Validated

Figure 4. A Novel Targets Was Validated

ICT1024, <u>a growth factor receptor like protein</u>

In vivo

In vitro
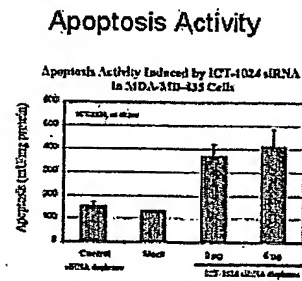
ICT-1024 siRNA mediated tumor growth inhibition
in MDA-MB-435/nude mice model

Apoptosis Activity

Apoptosis Activity Induced by ICT-1024 siRNA
in MDA-MD-435 Cells
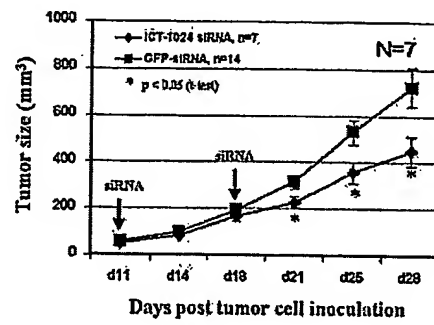
Figure 5.

ICT1025, a tumor reject antigen

In vivo
In vitro
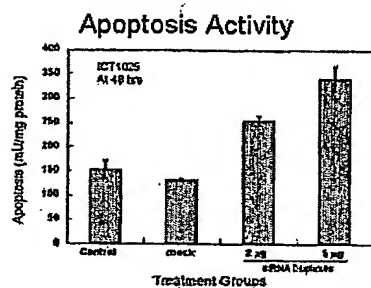
Xenograft tumor Inhibition
MDA-MB-435 cell induced tumor
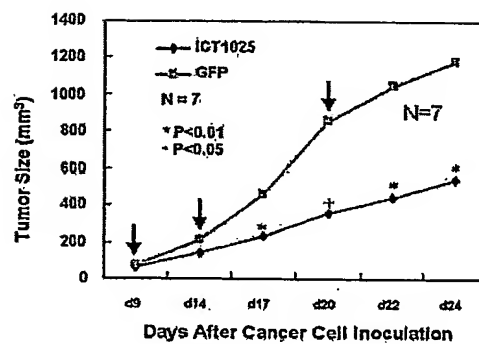
Figure 6.

Figure 7

ICT-1024 siRNA Design:

hEGFR-RP
(mRNA, 2964 bp)

ATG, 113   TGA 2678

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173 aagctggacattccctctgcg
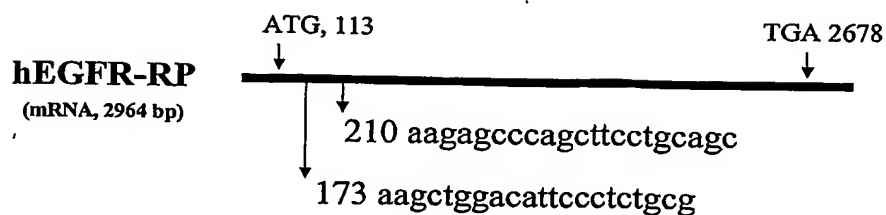
Figure 8.

ICT-1024 siRNA mediated tumor growth inhibition in MDA-MB-435/nude mice model
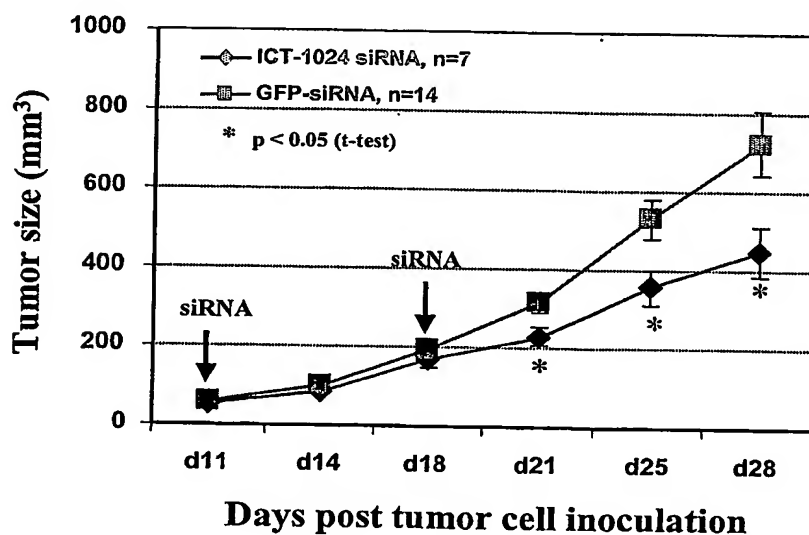

Days post tumor cell inoculation

Figure 9.

Apoptosis Activity Induced by ICT-1024 siRNA in MDA-MB-435 Cells

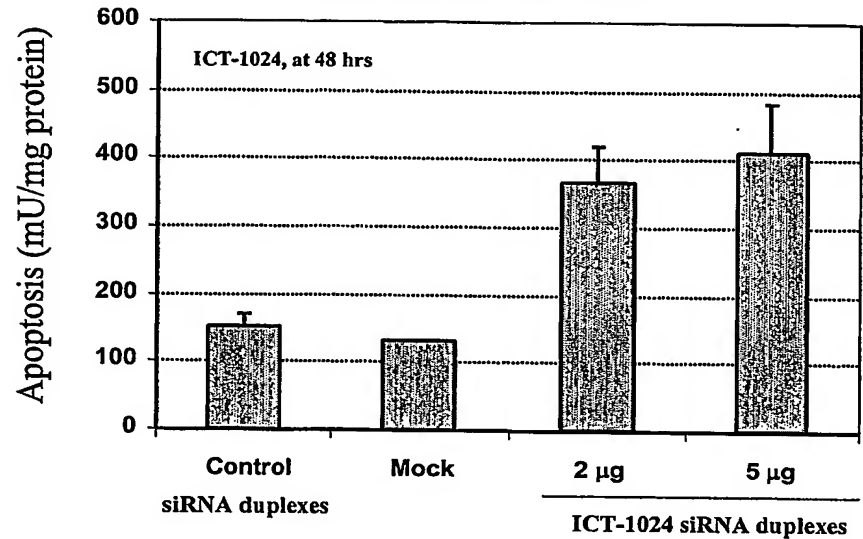
Figure 10.   SAGE/Microarray Data

CGAP SAGE
Expression Data
and Correlation:
ICT1024 has
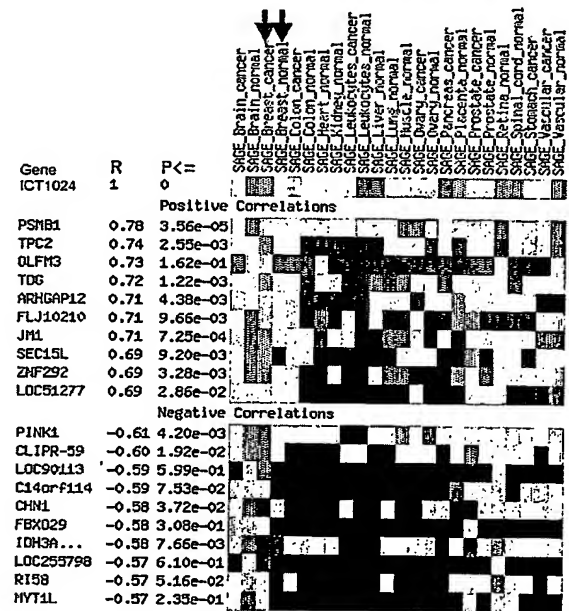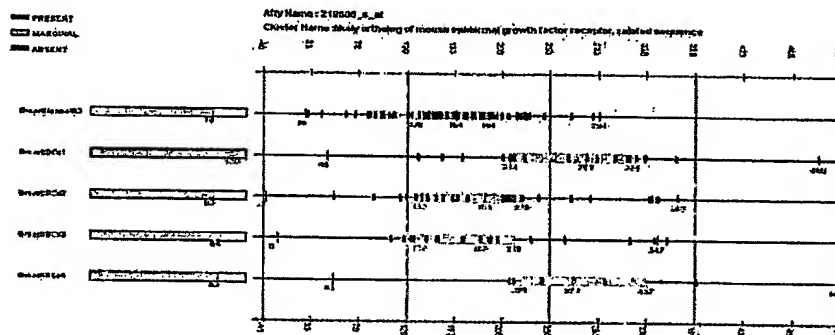significantly
positive correlation
with other breast
cancer genes

Figure 11 **Cancer Tissue Distribution**

ICT1024 is highly up regulated in all Stage I Breast Tumor samples (100%)

Figure 12. Consensus in rhomboid family

```
                                    10        20        30        40        50        60
                                 ....*....|....*....|....*....|....*....|....*....|....*....|
Human    consensus    1         PLQPGQLWR--LITSMFLHAGILHLLFNMLSLLFFGIPLERRLGSVRFLLLYLLSGLAG- 57
Yeast    gi 9963865    99        ALRNWQVYR--LVTYIFVYENPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIPAIFS- 155
Bacteria gi 3738201    47        LLQKRQLYE--IITYVTLHLSMLHIVFNFVSLLPAMSQFEKKQGTLACILVTVIPYTLFp 104
Yeast    gi 1653749    49        PRSLEGLRG--IVFAPFLHADFGHLIANSVPFVVLAWLVMLQ-EVSDFWIVTIITMVVG- 104
Human    gi 13621505   60        sksnarpvvaigdsDIYSYRIWS-FFCQWINTIPCWSNRRRPLGLTPFLLLYVLSGVhG- 117
Bacteria gi 20139804   103       PEIGREEAWR--FISYMLVHAgVQHILGNLCMQLVLGIPLEMVHKGLRVGLVYLAGVIAG- 159
Human    gi 1169951    129       PTLKPEFWR--YFTHALMHPSLMHILFNLLWWHYLGGAVEKRLGSGKLIVIRSISALLS- 185
Bacteria gi 11066250   198       SNPASKVLCspMLLSTFSHFSLPHMAANMYVLWSFSSSIVNILGQEQFMAVYLSAGVIS- 256
Human    gi 13813618   68        yLVIKGYYSe-LFTSIFITNSFVDPIFNFISLYVIYLIFGSRAGKHEYGIPILAGILGN- 125
Plant    gi 9294149    242       IFKHKDLKR--LFLSAFYHVNEPHLVYNMtSLLWKGIKLETSMGSSEFASMVPTLIGMS- 298

                                    70        80        90        100       110       120
                                 ....*....|....*....|....*....|....*....|....*....|....*....|
Human    consensus    58        SLLSLLLSPAS-----TPSVGASGAIFGLLGALLVLLPlNRILLLNP--GAALFLLLGII 110
Yeast    gi 9963865    156       AIIFLSPEAVSs----LSKLGEVEDARGFTPVAFAMLGVTTVRSRMRraLVFGMVVPSVL 211
Bacteria gi 3738201    105       GIMHLIVYHFPlrkdyVSIAGLSGWAFAFISASCVHSPQRLISFFN-----LFSIPAYCF 159
Yeast    gi 1653749    105       GLGVWLIAPPN-----TVTVGASILIFGYLGPLLFRGWFQKNLASIV1-SIVVLVLYGSA 158
Human    gi 13621505   118       NAFTFWLTPETV------AAGASTSLFGLPAAIVVLSFLGKNQALKD1-GKSYQTLIV-V 169
Bacteria gi 20139804   160       SLASSIFDPLR------YLVGASGGVYALMGGYFMNVLVNFQEMIPA--FGIPRLLIIIL 211
Human    gi 1169951    186       GYVQQKFSGPW-------FGGLSGVVYALMGYVWLRGERDPQSG--------IYLQRGLI 230
Bacteria gi 11066250   257       NFVSYLGKVATgr--yGPSLGASGAIMTVLAAVCTKIPEGR-LA--------IIFLPMFTF 306
Human    gi 13813618   126       LLTVIFYSPFT------LSSGASGGIFGLLSYYTFYDFLKKDNLG----VYGLVFLVSVP 175
Plant    gi 9294149    299       QGVTLLLAKSL-----LLLPDYDRAYYNEYAVGPSGVLFAMKVVLNSq-AEDYSSVYGIL 352

                                    130       140       150       160       170
                                 ....*....|....*....|....*....|....*....|....*....|.
Human    consensus    111       LLWLLLGL---LPGISNFG-----------HLGGLLAGLLLGPLLLRRPR 146
Yeast    gi 9963865    212       VPWLLLGAswlIPQTSFLS-----------NVCGLSIGLAYAHLLLFHRP 250
Bacteria gi 3738201    160       PIIYLIMTtilVPKASFIG-----------HASGAVMGYCTPFMLGSIPL 198
Yeast    gi 1653749    159       LWGLLPGR----AGVSWQG-----------HLFGFIGGAIAAWLIAREKH 193
Human    gi 13621505   170       NLLMNLF----MPNVSMAG-----------HIGGVVGGALLSIVFPTKMR 204
Bacteria gi 20139804   212       IIVLDMGF---ALYRRFFVpedgsp-vsfaaHIAGGPAGMSIGYTVPSCFD 258
Human    gi 1169951    231       IFALIWIV---AGWFDLFGmsma-----ngaHIAGLAVGLAMAFVDSLNAR 273
Bacteria gi 11066250   307       TAGNALKA---IIAMDTAGmilgwkffdhaaHLGGALFGIWYVTYGHELIW 354
Human    gi 13813618   176       GVSDLIPP-----NVNVVA-----------HIGGILGGIMYAVVYLIRS 209
Plant    gi 9294149    353       VPTKYAAWa-eLILVQMFVpnas-----flgHLGGILAGIIYLKLKGSYSG 397
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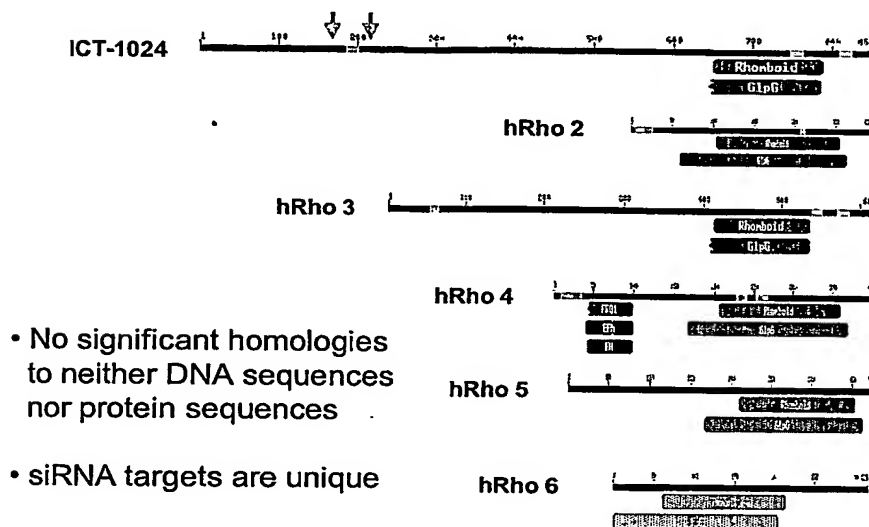
Figure 13.

Human rhomboid Proteins

Human Rhomboid Family Protein Alignments

Figure 14. **Function Domain Homology**

ICT-1024, A Novel Member of Rhomboid Family

ICT-1024

hRho 2

hRho 3

hRho 4

• No significant homologies
  to neither DNA sequences
  nor protein sequences

hRho 5

• siRNA targets are unique

hRho 6

Figure 15.   **Hydrophobicity Analysis**

Cellular Location and Topology predictions

TMHMM Model

TMpred Model
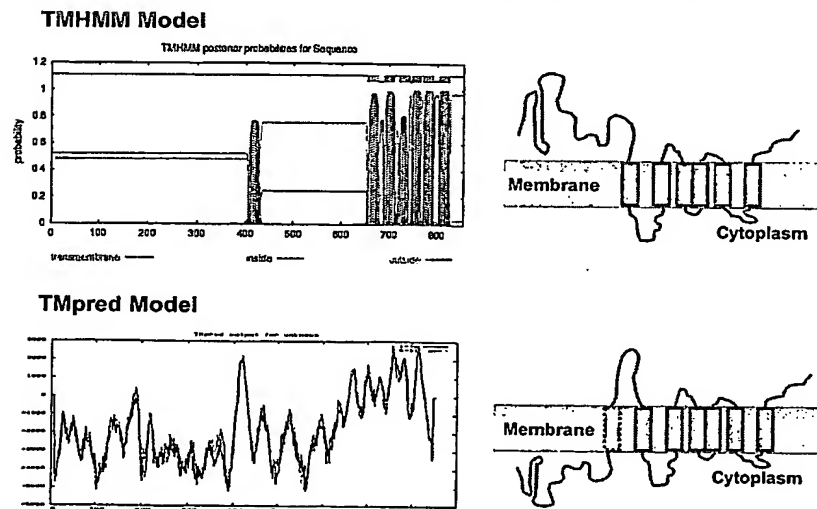
Activation of EGFRs and ligands

Figure 16.

ICT-1024 Intramembrane Protease Activity
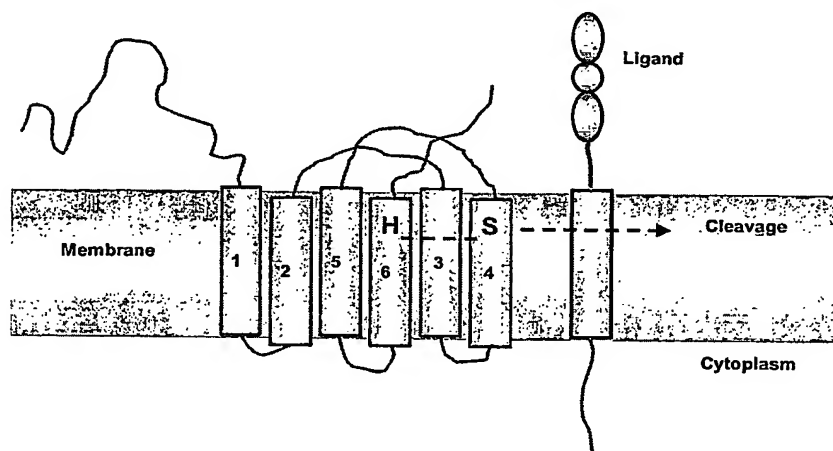
Refer to **Koonin EV, et al.** *Genome Biology, 2003*

Figure 17.
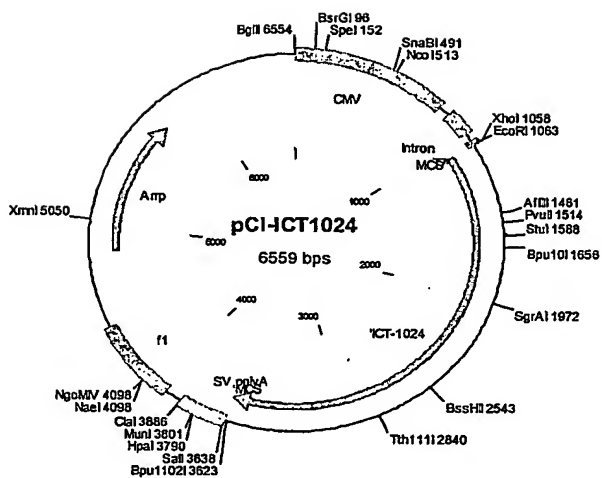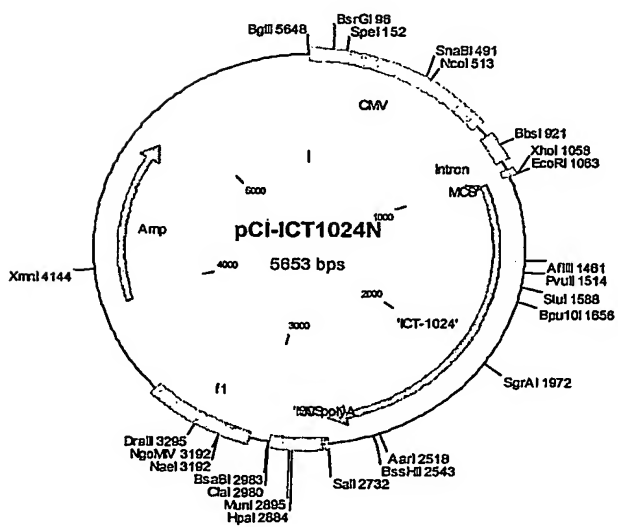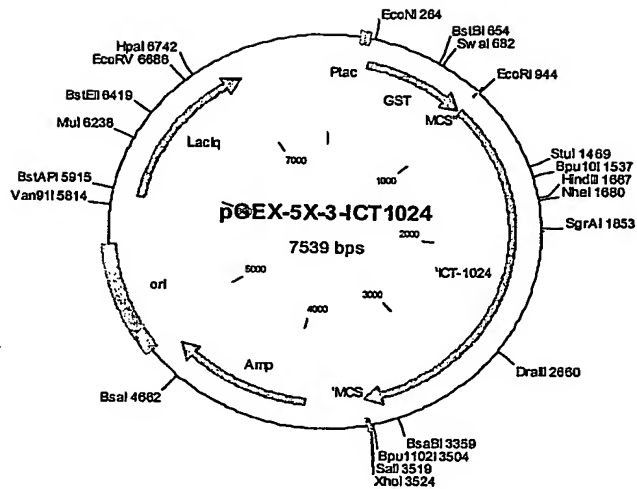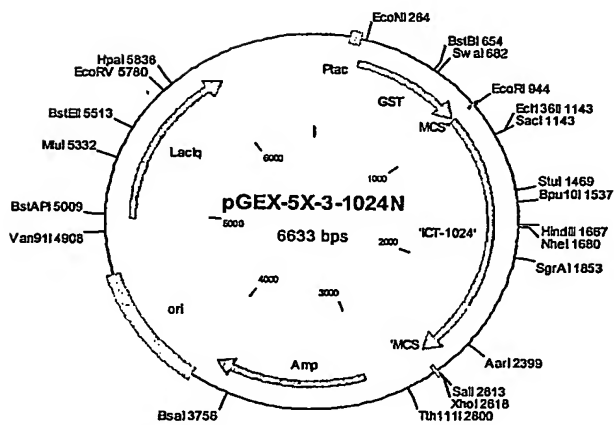

Figure 18.

Figure 19.
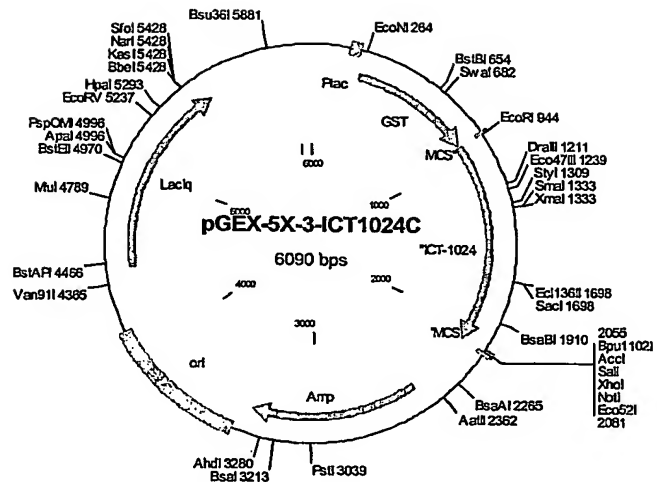

Figure 20.

Figure 21.

Figure 22.
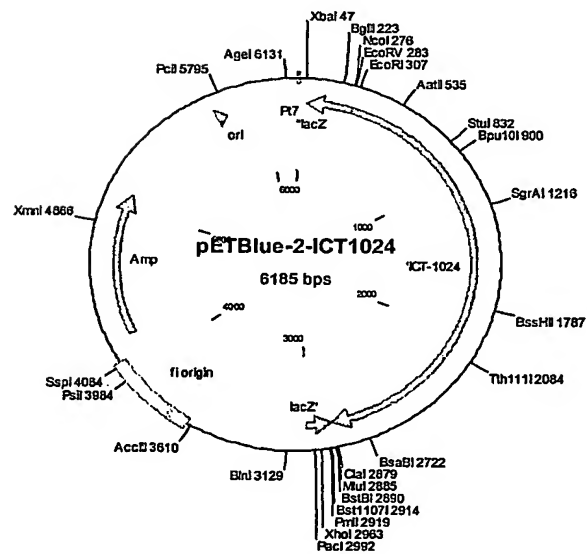
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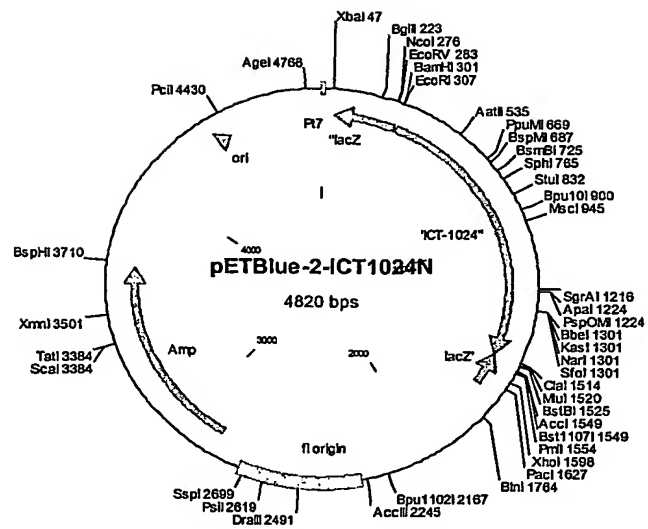
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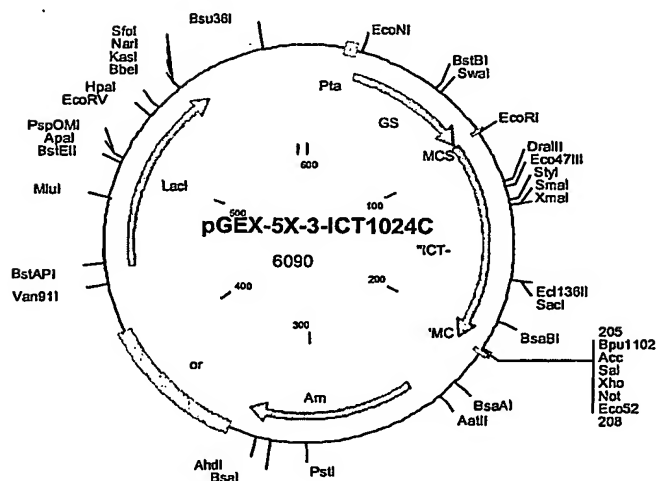
Fig. 25 (SEQ ID NO:58) ICT1024 PROTEIN (855 AA) CODING REGION: 1670-3637

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121   AATATGACCG CCATGTTGGC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG
181   GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC
241   GCCTGGCTGA CCGCCCCAACG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT
301   AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC GGTAAACTGC
361   CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGTCCG CCCCCTATTG ACGTCAATGA
421   CGGTAAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTACGGGACT TTCCTACTTG
481   GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAC
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1201  GGCTTTCCTG AGGAGTGTGA GTATGCCAGC CGAGACAGCC CACATCTCTT CACCCCACCA

1261  TGAGCTCCGG CGGCCGGTGC TGCAACGCCA GACGTCCATC ACACAGACCA TCCGCAGGGG

1321  GACCGCCGAC TGGTTTGGAG TGAGCAAGGA CAGTGACAGC ACCCAGAAAT GGCAGCGCAA

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1561  CTTCCGTGTG GCAGATGACA CTGCGGAAGG CCTGAGTGCC CCACACACTC CCGTCACGCC

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2041  GCGGAAGCAG AAGGAGGGCG CCGCAGCCCC GCAGCCCAAG GTGCGGCTCC GACAGGAGGT

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5761    ATTGATTTAA  AACTTCATTT  TTAATTTAAA  AGGATCTAGG  TGAAGATCCT  TTTTGATAAT

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Fig. 26 (SEQ ID NO:60) ICT1024 N TERMINUS 553 AA CODING REGION: 1070-2731

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181   GTCATTAGTT  CATAGCCCAT  ATATGGAGTT  CCGCGTTACA  TAACTTACGG  TAAATGGCCC
241   GCCTGGCTGA  CCGCCCAACG  ACCCCCGCCC  ATTGACGTCA  ATAATGACGT  ATGTTCCCAT
301   AGTAACGCCA  ATAGGGACTT  TCCATTGACG  TCAATGGGTG  GAGTATTTAC  GGTAAACTGC
361   CCACTTGGCA  GTACATCAAG  TGTATCATAT  GCCAAGTCCG  CCCCCTATTG  ACGTCAATGA
421   CGGTAAATGG  CCCGCCTGGC  ATTATGCCCA  GTACATGACC  TTACGGGACT  TTCCTACTTG
481   GCAGTACATC  TACGTATTAG  TCATCGCTAT  TACCATGGTG  ATGCGGTTTT  GGCAGTACAC
541   CAATGGGCGT  GGATAGCGGT  TTGACTCACG  GGGATTTCCA  AGTCTCCACC  CCATTGACGT
601   CAATGGGAGT  TTGTTTTGGC  ACCAAAATCA  ACGGGACTTT  CCAAAATGTC  GTAATAACCC
661   CGCCCCGTTG  ACGCAAATGG  GCGGTAGGCG  TGTACGGTGG  GAGGTCTATA  TAAGCAGAGC
721   TCGTTTAGTG  AACCGTCAGA  TCACTAGAAG  CTTTATTGCG  GTAGTTTATC  ACAGTTAAAT
781   TGCTAACGCA  GTCAGTGCTT  CTGACACAAC  AGTCTCGAAC  TTAAGCTGCA  GAAGTTGGTC
841   GTGAGGCACT  GGGCAGGTAA  GTATCAAGGT  TACAAGACAG  GTTTAAGGAG  ACCAATAGAA
901   ACTGGGCTTG  TCGAGACAGA  GAAGACTCTT  GCGTTTCTGA  TAGGCACCTA  TTGGTCTTAC
961   TGACATCCAC  TTTGCCTTTC  TCTCCACTCC  CAGTTCAATT  ACAGCTCTTA
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1021  AGGCTAGAGT  ACTTAATACG  ACTCACTATA  GGGCTAGCCTC  GAGAATTCCA  TGAGTGAGGC
1081  CCGCAGGGAC  AGCACGAGCA  GCCTGCAGCG  CAAGAAGCCA   CCCTGGCTAA  AGCTGGACAT
1141  TCCCTCTGCG  GTGCCCCTGA  CGGCAGAAGA  GCCCAGCTTC   CTGCAGCCCC  TGAGGCGACA
1201  GGCTTTCCTG  AGGAGTGTGA  GTATGCCAGC  CGAGACAGCC   CACATCTCTT  CACCCCACCA
1261  TGAGCTCCGG  CGGCCGGTGC  TGCAACGCCA  GACGTCCATC   ACACAGACCA  TCCGCAGGGG
1321  GACCGCCGAC  TGGTTTGGAG  TGAGCAAGGA  CAGTGACAGC   ACCCAGAAAT  GGCAGCGCAA
1381  GAGCATCCGT  CACTGCAGCC  AGCGCTACGG  GAAGCTGAAG   CCCCAGGTCC  TCCGGGAGCT
1441  GGACCTGCCC  AGCCAGGACA  ACGTGTCGCT  GACCAGCACC   GAGACGCCAC  CCCCACTCTA
1501  CGTGGGGCCA  TGCCAGCTGG  GCATGCAGAA  GATCATAGAC   CCCCTGCCCC  GTGGCCGTGC
1561  CTTCCGTGTG  GCAGATGACA  CTGCGGAAGG  CCTGAGTGCC   CCACACACTC  CCGTCACGCC
1621  GGGTGCTGCC  TCCCTCTGCT  CCTTCTCCAG  CTCCCGCTCA   GGTTTCCACC  GGCTCCCGCG
1681  GCGGCGCAAG  CGAGAGTCGG  TGGCCAAGAT  GAGCTTCCGG   GCGGCCGCAG  CGCTGATGAA
1741  AGGCCGCTCC  GTTAGGGATG  GCACCTTTCG  CCGGGGCACGG  CGTCGAAGCT  TCACTCCAGC
1801  TAGCTTTCTG  GAGGAGGACA  CAACTGATTT  CCCCGATGAG   CTGGACACAT  CCTTCTTTGC
1861  CCGGGAAGGT  ATCCTCCATG  AAGAGCTGTC  CACATACCCG   GATGAAGTTT  TCGAGTCCCC
1921  ATCGGGAGGCA GCGCTAAAGG  ACTGGGAGAA  GGCACCGGAG   CAGGCGGACC  TCACCGGCGG
1981  GGCCCTGGAC  CGCAGCGAGC  TTGAGCGCAG  CCACCTGCAG   CTGCCCCTGG  AGCGAGGCTG
2041  GCGGAAGCAG  AAGGAGGGCG  CCCGCAGCCCC GCAGCCCAAG   GTGCGGCTCC  GACAGGAGGT
2101  GGTGAGCACC  GCGGGGCCGC  GACGGGGCCCA GCGTATCGCG   GTGCCGGTGC  GCAAGCTCTT
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2161    CGCCCGGGAG AAGCGGCCGT ATGGGCTGGG CATGGTGGGA CGGCTCACCA ACCGCACCTA

2221    CCGCAAGCGC ATCGACACAGCT TCGTCAAGCG CCAGATCGAG GACATGGACG ACCACAGGCC

2281    CTTCTTCACC TACTGGCTTA CCTTCGTGCA CTCGCTCGTC ACCATCCTAG CCGTGTGCAT

2341    CTATGGCATC GCGCCCCGTGG GCTTCTCGCA GCATGAGACG GTGGACTCGG TGCTGCGGAA

2401    CCGCGGGGTC TACGAGAACG TCAAGTACGT GCAGCAGGAG AACTTCTGGA TCGGGCCCAG

2461    CTCGGAGGCC CTCATCCACC TGGGCGCCAA GTTTTCGCCC TGCATGCGCC AGGACCCGCA

2521    GGTGCACAGC TTCATTCGCT CGGCGCGGCGA GCGGCGAGAAG CACTCCGCCT GCTGCGGTGCG

2581    CAACGACAGG TCGGGCTGCG TGCAGACCTC GGAGGAGGAG TGCTCGTCCA CGCTGGCAGT

2641    GTGGGTGAAG TGGCCCATCC ATCCCAGCGC CCCAGAGCTT GCGGGGCCACA AGAGACAGTT

2701    TGGCTCTGTC TGCCACCAGG ATCCCAGGTG AGTCGACCCG GGCGGCGCGCT TCGAGCAGAC

2761    ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACACAACTA GAATGCAGTG AAAAAAATGC

2821    TTTATTTGTG AAATTTGTGA TGCTATTGCT TTATTTGTAA CCATTATAAG CTGCAATAAA

2881    CAAGTTAACA ACAACAATTG CATTCATTTT ATGTTTCAGG TTCAGGGGGA GATGTGGGAG

2941    GTTTTTTAAA GCAAGTAAAA CCTCTACAAA TGTGGTAAAA TCGATAAGGA TCCGGGGCTGG

3001    CGTAAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC

3061    GAATGGACGC GCCCTGTAGC GGCGCATTAA GCGCGGCGGG TGTGGTGGTT ACGGCGCAGCG

3121    TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT CGCTTTCTTC CCTTCCTTTC

3181    TCGCCACGTT CGCCGGCTTT CCCCGTCAAG CTCTAAATCG GGGGCTCCCT TTAGGGTTCC

3241    GATTTAGAGC TTTACGGCAC CTCGACCGCA AAAAACTTGA TTTGGGTGAT GGTTCACGTA
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3301  GTGGGCCATC GCCCTGATAG ACGGTTTTTC GCCCTTTGAC GTTGGAGTCC ACGTTCTTTA

3361  ATAGTGGACT CTTGTTCCAA ACTGGAACAA CACTCAACCC TATCTCGGTC TATTCTTTTG

3421  ATTTATAAGG GATTTTGCCG ATTTCGGCCT ATTGGTTAAA AAATGAGCTG ATTTAACAAA

3481  TATTTAACGC GAATTTTAAC AAAATATTAA CGTTTACAAT TTCGCCTGAT GCGGTATTTT

3541  CTCCTTACGC ATCTGTGCGG TATTTCACAC CGCATATGGT GCACTCTCAG TACAATCTGC

3601  TCTGATGCCG CATAGTTAAG CCAGCCCCGA CACCCGCCAA CACCCGCTGA CGCGCCCTGA

3661  CGGGCTTGTC TGCTCCCGGC ATCCGCTTAC AGACAAGCTG TGACCGTCTC CGGGAGCTGC

3721  ATGTGTCAGA GGTTTTCACC GTCATCACCG AAACGCGCGA GACGAAAGGG CCTCGTGATA

3781  CGCCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT CTTAGACGTC AGGTGGCACT

3841  TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG

3901  TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT

3961  ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT

4021  GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA

4081  CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC

4141  GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC

4201  CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG

4261  GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA

4321  TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC

4381  GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT
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4441  GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG
4501  CCTGTAGCAA TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT
4561  TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC
4621  TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGGTCT
4681  CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT CCCGTATCGT AGTTATCTAC
4741  ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC
4801  TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT
4861  TTAAAACTTC ATTTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG
4921  ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAAGATC
4981  AAAGGATCTT CTTGAGATCC TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAAA
5041  CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG
5101  GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA
5161  GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTTA
5221  CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC AAGACGATAG
5281  TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG
5341  GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG
5401  CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG
5461  CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC
5521  CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG CCTATGAAA
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5581  AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG

5641  GCTCGACAGA TCT
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Fig. 27, (SEQ ID NO: 61) ICT1024 coding region: 947-3518

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  1   TCGACTCGAG CGGCCGCGATC GTGACTGACT GACGATCTGC CTCGCGCGGTT TCGGTGATGA
 61   CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTTGTC TGTAAGCGGA
121   TGCCGGGGAGC AGACAAGCCC GTCAGGGCGC GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC
181   AGCCATGACC CAGTCACGTA GCGATAGCGG AGTGTATAAT TCTTGAAGAC GAAAGGGCCT
241   CGTGATACGC CTATTTTAT AGGTTAATGT CATGATAATA ATGGTTTCTT AGACGTCAGG
301   TGGCACTTTT CGGGGAAATG TGCGCGGAAC CCCTATTTGT TTATTTTCT AAATACATTC
361   AAATATGTAT CCGCTCATGA GACAATAACC CTGATAAATG CTTCAATAAT ATTGAAAAAG
421   GAAGAGTATG AGTATTCAAC ATTTCCGTGT CGCCCTTATT CCCTTTTTG CGGCATTTTG
481   CCTTCCTGTT TTTGCTCACC CAGAAACGCT GGTGAAAGTA AAAGATGCTG AAGATCAGTT
541   GGGTGCACGA GTGGGTTACA TCGAACTGGA TCTCAACAGC GGTAAGATCC TTGAGAGTTT
601   TCGCCCCGAA GAACGTTTTC CAATGATGAG CACTTTTAAA GTTCTGCTAT GTGGCGCGGT
661   ATTATCCCGT GTTGACGCCG GGCAAGAGCA ACTCGGTCGC CGCATACACT ATTCTCAGAA
721   TGACTTGGTT GAGTACTCAC CAGTCACAGA AAAGCATCTT ACGGATGGCA TGACAGTAAG
781   AGAATTATGC AGTGCTGCCA TAACCATGAG TGATAACACT GCGGCCAACT TACTTCTGAC
841   AACGATCGGA GGACCGAAGG AGCTAACCGC TTTTTTGCAC AACATGGGGG ATCATGTAAC
901   TCGCCTTGAT CGTTGGGAAC CGGAGCTGAA TGAAGCCATA CCAAACGACG AGCGTGACAC
961   CACGATGCCT GCAGCAATGG CAACAACGTT GCGCAAACTA TTAACTGGCG AACTACTTAC
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1021  TCTAGCTTCC CGGCAACAAT TAATAGACTG GATGGAGGCG GATAAAGTTG CAGGACCACT
1081  TCTGCGCTCG GCCCTTCCGG CTGGCTGGTT TATTGCTGAT AAATCTGGAG CCGGTGAGCG
1141  TGGGTCTCGC GGTATCATTG CAGCACTGGG GCCAGATGGT AAGCCCTCCC GTATCGTAGT
1201  TATCTACACG ACGGGGAGTC AGGCAACTAT GGATGAACGA AATAGACAGA TCGCTGAGAT
1261  AGGTGCCTCA CTGATTAAGC ATTGGTAACT GTCAGACCAA GTTTACTCAT ATATACTTTA
1321  GATTGATTTA AAACTTCATT TTTAATTTAA AAGGATCTAG GTGAAGATCC TTTTTGATAA
1381  TCTCATGACC AAAATCCCTT AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA
1441  AAAGATCAAA GGATCTTCTT GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC
1501  AAAAAAACCA CCGCTACCAG CGGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT
1561  TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA GATACCAAAT ACTGTCCTTC TAGTGTAGCC
1621  GTAGTTAGGC CACCACTTCA AGAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT
1681  CCTGTTACCA GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT CTTACCGGGT TGGACTCAAG
1741  ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACACAGCC
1801  CAGCTTGGAG CGAACGACCT ACACCGAACT GAGATACCTA CAGCGTGAGC TATGAGAAAG
1861  CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC
1921  AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG AAACGCCCTG TATCTTTATA GTCCTGTCGG
1981  GTTCGCCAC CTCTGACTTG AGCGTCGATT TTTGTGATGC TCGTCAGGGG GGCGGGAGCCT
2041  ATGGAAAAAC GCCAGCAACG CGGCCTTTTT ACGGTTCCTG GCCTTTTGCT GGCCTTTTGC
2101  TCACATGTTC TTTCCTGCGT TATCCCCTGA TTCTGTGGAT AACCGTATTA CCGCCTTTGA
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2161   GTGAGCTGAT ACCGCTCGCC GCAGCCGAAC GACCGAGCGC AGCGAGTCAG TGAGCGAGGA

2221   AGCGGAAGAG CGCCTGATGC GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG

2281   CATAAATTCC GACACCATCG AATGGTGCAA AACCTTTCGC GGTATGGCAT GATAGCGCCC

2341   GGAAGAGAGT CAATTCAGGG TGGTGAATGT GAAACCAGTA ACGTTATACG ATGTCGCAGA

2401   GTATGCCGGT GTCTCTTATC AGACCGTTTC CCGCGTGGTG AACCAGGCCA GCCACGTTTC

2461   TGCGAAAACG CGGGAAAAAG TGGAAGCGGC GATGGCGCGAG CTGAATTACA TTCCCAACCG

2521   CGTGGCACAA CAACTGGCGG GCAAACAGTC GTTGCTGATT GGCGTTGCCA CCTCCAGTCT

2581   GGCCCTGCAC GCGCCGTCGC AAATTGTCGC GGCGATTAAA TCTCGCGCCG ATCAACTGGG

2641   TGCCAGCGTG GTGGTGTCGA TGGTAGAACG AAGCGGCGTC GAAGCCTGTA AAGCGGCGGT

2701   GCACAATCTT CTCGCGCAAC GCGTCAGTGG GCTGATCATT AACTATCCGC TGGATGACCA

2761   GGATGCCATT GCTGTGGAAG CTGCCTGCAC TAATGTTCCG GCGTTATTTC TTGATGTCTC

2821   TGACCAGACA CCCATCAACA GTATTATTTT CTCCCATGAA GACGGTACGC GACTGGGCGT

2881   GGAGCATCTG GTCGCATTGG GTCACCAGCA AATCGCGCTG TTAGCGGGCC CATTAAGTTC

2941   TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG GCATAAATAT CTCACTCGCA ATCAAATTCA

3001   GCCGATAGCG GAACGGGAAG GCGACTGGAG TGCCATGTCC GGTTTTCAAC AAACCATGCA

3061   AATGCTGAAT GAGGGCATCG TTCCCACTGC GATGCTGGTT GCCAACGATC AGATGGCGCT

3121   GGGCGCAATG CGCGCCATTA CCGAGTCCGG GCTGCGCGTT GGTGCGGATA TCTCGGTAGT

3181   GGGATACGAC GATACCGAAG ACAGCTCATG TTATATCCCG CCGTTAACCA CCATCAAACA

3241   GGATTTTCGC CTGCTGGGGC AAACCAGCGT GGACCGCTTG CTGCAACTCT CTCAGGGCCA
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3301  GGCGGTGAAG  GGCAATCAGC  TGTTGCCCGT  CTCACTGGTG  AAAAGAAAAA  CCACCCTGGC
3361  GCCCAATACG  CAAACCGCCT  CTCCCCGCGC  GTTGGCCGAT  TCATTAATGC  AGCTGGCACG
3421  ACAGGTTTCC  CGACTGGAAA  GCGGGCAGTG  AGCGCAACGC  AATTAATGTG  AGTTAGCTCA
3481  CTCATTAGGC  ACCCCAGGCT  TTACACTTTA  TGCTTCCGGC  TCGTATGTTG  TGTGGAATTG
3541  TGAGCGGATA  ACAATTTCAC  ACAGGAAACA  GCTATGACCA  TGATTACGGA  TTCACTGGCC
3601  GTCGTTTTAC  AAGTCGTGA   CTGGGAAAAC  CCTGGCGTTA  CCCAACTTAA  TCGCCTTGCA
3661  GCACATCCCC  CTTTCGCCAG  CTGGCGTAAT  AGCGAAGAGG  CCCGCACCGA  TCGCCCTTCC
3721  CAACAGTTGC  GCAGCCTGAA  TGGCGAATGG  CGCTTTGCCT  GGTTTCCGGC  ACCAGAAGCG
3781  GTGCCGGAAA  GCTGGCTGGA  GTGCGATCTT  CCTGAGGCCG  ATACTGTCGT  CGTCCCCTCA
3841  AACTGGCAGA  TGCACGGTTA  CGATGCGCCC  ATCTACACCA  ACGTAACCTA  TCCCATTACG
3901  GTCAATCCGC  CGTTTGTTCC  CACGGAGAAT  CCGACGGGTT  GTTACTCGCT  CACATTTAAT
3961  GTTGATGAAA  GCTGGCTACA  GGAAGGCCAG  ACGCGAATTA  TTTTTGATGG  CGTTGGAATT
4021  AGCTTATCGA  CTGCACGGTG  CACCAATGCT  TCTGGCGTCA  GGCAGCCATC  GGAAGCTGTG
4081  GTATGGCTGT  GCAGGTCGTA  AATCACTGCA  TAATTCGTGT  CGCTCAAGGC  GCACTCCCGT
4141  TCTGGATAAT  GTTTTTTGCG  CCGACATCAT  AACGGTTCTG  GCAAATATTC  TGAAATGAGC
4201  TGTTGACAAT  TAATCATCGG  CTCGTATAAT  GTGTGGAATT  GTGAGCGGAT  AACAATTTCA
4261  CACAGGAAAC  AGTATTCATG  TCCCCTATAC  TAGGTTATTG  GAAAATTAAG  GGCCTTGTGC
4321  AACCCACTCG  ACTTCTTTTG  GAATATCTTG  AAGAAAAATA  TGAAGAGCAT  TTGTATGAGC
4381  GCGATGAAGG  TGATAAATGG  CGAAACAAAA  AGTTTGAATT  GGGTTTGGAG  TTTCCCAATC
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4441  TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA
4501  TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC
4561  TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT
4621  TTGAAACTCT CAAAGTTGAT TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG
4681  ATCGTTTATG TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT
4741  TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA
4801  AATTAGTTTG TTTTAAAAAA CGTATTGAAG CTATCCCACA AATTGATAAG TACTTGAAAT
4861  CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
4921  ATCCTCCAAA ATCGGATCTG ATCGAAGGTC GTGGGATCCC CAGG
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FIG. 28, (SEQ ID NO: 62) ICT1024 N terminus 553 aa coding region: 947-2600

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1     AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
61    GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT
121   TCTTGGATAAT GTTTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC
181   TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA
241   CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC
301   AACCCACTCG ACTTCTTTTG GAATATCTTG AAGAAAAATA TGAAGAGCAT TTGTATGAGC
361   GCGATGAAGG TGATAAAATGG CGAAACAAAA AGTTTGAATT GGGTTTGGAG TTTCCCAATC
421   TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA
481   TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC
541   TTGAAGGAGC GGTTTTGGAT ATTAGAATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT
601   TTGAAACTCT CAAAGTTGAT TTTCTTAGCA TATTTAAATG ATGTTCGAAA ATGTTCGAAG
661   ATCGTTTATG TCATAAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT
721   TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA
781   AATTAGTTTG TTTTAAAAAA CGTATTGAAG CTATCCCACA AATTGATAAG TACTTGAAAT
841   CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
901   ATCCTCCAAA ATCGGATCTG ATCGAAGGTC GTGGGATCCC CAGGAATTCC ATGAGTGAGG
961   CCCGCAGGGA CAGCACGAGC CAGCCTGCAGC GCAAGAAGCC ACCCTGGCTA AAGCTGGACA
1021  TTCCCTCTGC GGTGCCCCTG ACGGCAGAAG AGCCCAGCTT CCTGCAGCCC CTGAGGCGAC
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1081  AGGCTTTCCT  GAGGAGTGTG  AGTATGCCAG  CCGAGACAGC  CCACATCTCT  TCACCCCACC
1141  ATGAGCTCCG  GCGGCCGGTG  CTGCAACGCC  AGACGTCCAT  CACACAGACC  ATCCGCAGGG
1201  GGACCGCCGA  CTGGTTTGGA  GTGAGCAAGG  ACAGTGACAG  CACCCAGAAA  TGGCAGCGCA
1261  AGAGCATCCG  TCACTGCAGC  CAGCGCTACG  GGAAGCTGAA  GCCCCAGGTC  CTCCGGGGAGC
1321  TGGACCTGCC  CAGCCAGGAC  AACGTGTCGC  TGACCAGCAC  CGAGACGCCA  CCCCCACTCT
1381  ACGTGGGGCC  ATGCCAGCTG  GGCATGCAGA  AGATCATAGA  CCCCCTGGCC  CGTGGCCGTG
1441  CCTTCCGTGT  GGCAGATGAC  ACTGCGGAAG  GCCTGAGTGC  CCCACACACT  CCCGTCACGC
1501  CGGGTGCTGC  CTCCCTCTGC  TCCTTCTCCA  GCTCCCGCTC  AGGTTTCCAC  CGGCTCCCGC
1561  GGCGGCGCAA  GCGAGAGTCG  GTGGCCAAGA  TGAGCTTCCG  GGCGGCCGCA  GCGGCTGATGA
1621  AAGGCCGCTC  CGTTAGGGAT  GGCACCTTTC  GCCGGGGCACG  GCGTCGAAGC  TTCACTCCAG
1681  CTAGCTTTCT  GGAGGAGGAC  ACAACTGATT  TCCCCGATGA  GCTGGACACA  TCCTTCTTTG
1741  CCCGGGAAGG  TATCCTCCAT  GAAGAGCTGT  CCACATACCC  GGATGAAGTT  TTCGAGTCCC
1801  CATCGGAGGC  AGCGCTAAAG  GACTGGGAGA  AGGCACCGGA  GCAGGCGGAC  CTCACCGGCG
1861  GGGCCCTGGA  CCGCAGCGAG  CTTGAGCGCA  GCCACCTGAT  GCTGCCCTTG  GAGCGGAGGCT
1921  GGCGGAAGCA  GAAGGAGGGC  GCCGCAGCCC  CGCAGGGCCA  GGTGCGGCTC  CGACAGGAGG
1981  TGGTGAGCAC  CGCGGGGCCG  CGACGGGGCCG  AGCGTATCGC  GGTGCCGGTG  CGCAAGCTCT
2041  TCGCCCCGGGA  GAAGCGGCCG  TATGGGCTGG  GCATGGTGGG  ACGGCTCACC  AACCGCACCT
2101  ACCGCAAGCG  CATCGACAGC  TTCGTCAAGC  GCCAGATCGA  GGACATGGAC  GACCACAGGC
2161  CCTTCTTCAC  CTACTGGCTT  ACCTTCGTGC  ACTCGCTCGT  CACCATCCTA  GCCGTGTGCA
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2221   TCTATGGCAT CGCGCCCGTG GGCTTCTCGC AGCATGAGAC GGTGGACTCG GTGCTGCGGA
2281   ACCGCGGGGT CTACGAGAAC GTCAAGTACG TGCAGCAGGA GAACTTCTGG ATCGGGCCCA
2341   GCTCGGAGGC CCTCATCCAC CTGGGCGCCA AGTTTTCGCC CTGCATGCGC CAGGACCCGC
2401   AGGTGCACAG CTTCATTCGC TCGGCGGCGG AGCGCGGAGAA GCACTCCGCC TGCTGCGTGC
2461   GCAACGACAG GTCGGGCTGC GTGCAGACCT CGGAGGAGGA GTGCTCGTCC ACGCTGGCAG
2521   TGTGGGTGAA GTGGCCCATC CATCCCAGCG CCCCAGAGCT TGCGGGGCCAC AAGAGACAGT
2581   TTGGCTCTGT CTGCCACCAG GATCCCAGGT GAGTCGACTC GAGCGGCCGC ATCGTGACTG
2641   ACTGACGATC TGCCTCGCGC GTTTCGGTGA TGACGGTGAA AACCTCTGAC ACATGCAGCT
2701   CCCGGAGACG GTCACAGCTT GTCTGTAAGC GGATGCCGGG AGCAGACAAG CCCGTCAGGG
2761   CGCGTCAGCG GGTGTTGGCG GGTGTCGGGG CGCAGCCATG ACCCAGTCAC GTAGCGATAG
2821   CGGAGTGTAT AATTCTTGAA GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA
2881   TGTCATGATA ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG
2941   AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA
3001   ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG
3061   TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC
3121   GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT
3181   GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT
3241   GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG CCGGGCAAGA
3301   GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC
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3361    AGAAAAGCAT    CTTACGGATG    GCATGACAGT    AAGAGAATTA    TGCAGTGCTG    CCATAACCAT

3421    GAGTGATAAC    ACTGCGGCCA    ACTTACTTCT    GACAACGATC    GGAGGACCGA    AGGAGCTAAC

3481    CGCTTTTTG     CACAACATGG    GGGATCATGT    AACTCGCCTT    GATCGTTGGG    AACCGGAGCT

3541    GAATGAAGCC    ATACCAAACG    ACGAGGGTGA    CACCACGATG    CCTGCAGCAA    TGGCAACAAC

3601    GTTGCGCAAA    CTATTAACTG    GCGAACTACT    TACTCTAGCT    TCCCGGCAAC    AATTAATAGA

3661    CTGGATGGAG    GCGGATAAAG    TTGCAGGACC    ACTTCTGCGC    TCGGCCCTTC    CGGCTGGCTG

3721    GTTTATTGCT    GATAAATCTG    GAGCCGGTGA    GCGTGGGTCT    CGCGGTATCA    TTGCAGCACT

3781    GGGGCCAGAT    GGTAAGCCCT    CCCGTATCGT    AGTTATCTAC    ACGACGGGGA    GTCAGGCAAC

3841    TATGGATGAA    CGAAATAGAC    AGATCGCTGA    GATAGGTGCC    TCACTGATTA    AGCATTGGTA

3901    ACTGTCAGAC    CAAGTTTACT    CATATATACT    TTAGATTGAT    TTAAAACTTC    ATTTTTAATT

3961    TAAAAGGATC    TAGGTGAAGA    TCCTTTTTGA    TAATCTCATG    ACCAAAATCC    CTTAACGTGA

4021    GTTTTCGTTC    CACTGAGCGT    CAGACCCCGT    AGAAAAGATC    AAAGGATCTT    CTTGAGATCC

4081    TTTTTTTCTG    CGCGTAATCT    GCTGCTTGCA    AACAAAAAAA    CCACCGCTAC    CAGCGGTGGT

4141    TTGTTTGCCG    GATCAAGAGC    TACCAACTCT    TTTTCCGAAG    GTAACTGGCT    TCAGCAGAGC

4201    GCAGATACCA    AATACTGTCC    TTCTAGTGTA    GCCGTAGTTA    GGCCACCACT    TCAAGAACTC

4261    TGTAGCACCG    CCTACATACC    TCGCTCTGCT    AATCCTGTTA    CCAGTGGCTG    CTGCCAGTGG

4321    CGATAAGTCG    TGTCTTACCG    GGTTGGACTC    AAGACGATAG    TTACCGGATA    AGGCGCAGCG

4381    GTCGGGCTGA    ACGGGGGGTT    CGTGCACACA    GCCCAGCTTG    GAGCGAACGA    CCTACACCGA

4441    ACTGAGATAC    CTACAGCGTG    AGCTATGAGA    AAGCGCCACG    CTTCCCGAAG    GGAGAAAGGC
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4501  GGACAGGTAT  CCGGTAAGCG  GCAGGGTCGG  AACAGGAGAG  CGCACGAGGG  AGCTTCCAGG
4561  GGGAAACGCC  TGGTATCTTT  ATAGTCCTGT  CGGGTTTCGC  CACCTCTGAC  TTGAGCGTCG
4621  ATTTTTGTGA  TGCTCGTCAG  GGGGGCGGAG  CCTATGGAAA  AACGCCAGCA  ACGCGGCCTT
4681  TTTACGGTTC  CTGGCCTTTT  GCTGGCCTTT  TGCTCACATG  TTCTTTCCTG  CGTTATCCCC
4741  TGATTCTGTG  GATAACCGTA  TTACCGCCTT  TGAGTGAGCT  GATACCGCTC  GCCGCAGCCG
4801  AACGACCGAG  CGCAGCGAGT  CAGTGAGCGA  GGAAGCGGAA  GAGCGCCTGA  TGCGGTATTT
4861  TCTCCTTACG  CATCTGTGCG  GTATTTCACA  CCGCATAAAT  TCCGACACCA  TCGAATGGTG
4921  CAAAACCTTT  CGCGGTATGG  CATGATAGCG  CCCGGAAGAG  AGTCAATTCA  GGGTGGTGAA
4981  TGTGAAACCA  GTAACGTTAT  ACGATGTCGC  AGAGTATGCC  GGTGTCTCTT  ATCAGACCGT
5041  TTCCCGCGTG  GTGAACCAGG  CCAGCCACGT  TTCTGCGAAA  ACGCGGGAAA  AAGTGGAAGC
5101  GGCGATGGCG  GAGCTGAATT  ACATTCCCAA  CCGCGTGGCA  CAACAACTGG  CGGGCAAACA
5161  GTCGTTGCTG  ATTGGCGTTG  CCACCTCCAG  TCTGGCCCTG  CACGCGCCGT  CGCAAATTGT
5221  CGCGGCGATT  AAATCTCGCG  CCGATCAACT  GGGTGCCAGC  GTGGTGGTGT  CGATGGTAGA
5281  ACGAAGCGGC  GTCGAAGCCT  GTAAAGCGGC  GGTGCACAAT  CTTCTCGCGC  AACGCGTCAG
5341  TGGGCTGATC  ATTAACTATC  CGCTGGATGA  CCAGGATGCC  ATTGCTGTGG  AAGCTGCCTG
5401  CACTAATGTT  CCGGCGTTAT  TTCTTGATGT  CTCTGACCAG  ACACCCATCA  ACAGTATTAT
5461  TTTCTCCCAT  GAAGACGGTA  CGCGACTGGG  CGTGGAGCAT  CTGGTCGCAT  TGGGTCACCA
5521  GCAAATCGCG  CTGTTAGCGG  GCCCATTAAG  TTCTGTCTCG  GCGCGTCTGC  GTCTGGCTGG
5581  CTGGCATAAA  TATCTCACTC  GCAATCAAAT  TCAGCCGATA  GCGGAACGGG  AAGGGCACTG
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5641  GAGTGCCATG TCCGGTTTTC AACAAACCAT GCAAATGCTG AATGAGGGCA TCGTTCCCAC
5701  TGCGATGCTG GTTGCCAACG ATCAGATGGC GCTGGGCGCA ATGCCGCGCCA TTACCGAGTC
5761  CGGGCTGCGC GTTGGTGCGG ATATCTCGGT AGTGGGATAC GACGATACCG AAGACAGCTC
5821  ATGTTATATC CCGCCGTTAA CCACCATCAA ACAGGATTTT CGCCTGCTGG GGCAAAACCAG
5881  CGTGGACCGC TTGCTGCAAC TCTCTCAGGG CCAGGCGGTG AAGGGCAATC AGCTGTTGCC
5941  CGTCTCACTG GTGAAAAGAA AAACCACCCT GGCGCCCAAT ACGCAAAACCG CCTCTCCCCG
6001  CGCGGTTGGCC GATTCATTAA TGCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA
6061  GTGAGCGCAA CGCAATTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT
6121  TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA
6181  ACAGCTATGA CCATGATTAC GGATTCACTG GCCGTCGTTT TACAACGTCG TGACTGGGAA
6241  AACCCTGGCG TTACCCAACT TAATCGCCTT GCAGCACATC CCCCTTTCGC CAGCTGGCGT
6301  AATAGCGAAG AGGCCCGCAC CGATCGCCCT TCCCAACAGT TGCGCAGCCT GAATGGCGAA
6361  TGGCGCTTTG CCTGGTTTCC GGCACCAGAA GCGGTGCCGG AAAGCTGGCT GGAGTGCGAT
6421  CTTCCTGAGG CCGATACTGT CGTCGTCCCC TCAAACTGGC AGATGCACGG TTACGATGCG
6481  CCCATCTACA CCAACGTAAC CTATCCCATT ACGGTCAAATC CGCCGTTTGT TCCCACGGAG
6541  AATCCGACGG GTTGTTACTC GCTCACATTT AATGTTGATG AAAGCTGGCT ACAGGAAGGC
6601  CAGACGCGAA TTATTTTTGA TGGCGTTGGA ATT
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FIG. 29, (SEQ ID NO:64) Coding region for the C terminus 375 aa: 945-2069

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   1   AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
  61   GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT
 121   TCTGGATAAT GTTTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC
 181   TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGTGGAATT GTGAGCGGAT AACAATTTCA
 241   CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC
 301   AACCCACTCG ACTTCTTTTG GAATATCTTG AAGAAAAATA TGAAGAGCAT TTGTATGAGC
 361   GCGATGAAGG TGATAAATGG CGAAACAAAA AGTTTGAATT GGGGTTTGGAG TTTCCCAATC
 421   TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA
 481   TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC
 541   TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT
 601   TTGAAACTCT CAAAGTTGAT TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG
 661   ATCGTTTATG TCATAAAACA TATTAAAATG GTGATCATGT AACCCATCCT GACTTCATGT
 721   TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA
 781   AATTAGTTTG TTTTAAAAAA CGTATTGAAG CTATCCCACA AATTGATAAG TACTTGAAAT
 841   CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
 901   ATCCTCCAAA ATCGGATCTG ATCGAAGGTC GTGGGATCCC CAGGAATTCC CAGGTGCACA
 961   GCTTCATTCG CTCGGCGCGC GAGCGCGAGA AGCACTCCGC CTGCTGCGTG CGCAACGACA
1021   GGTCGGGGCTG CGTGCAGACC TCGGAGGAGG AGTGCTCGTC CACGCTGGCA GTGTGGGGTGA
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1081   AGTGGCCCAT CCATCCCAGC GCCCCAGAGC TTGCGGGGCCA CAAGAGACAG TTTGGCTCTG

1141   TCTGCCACCA GGATCCCAGG GTGTGTGATG AGCCCTCCTC CGAAGACCCT CATGAGTGGC

1201   CAGAAGACAT CACCAAGTGG CCGATCTGCA CCAAAAAACAG CGCTGGGAAC CACACCAACC

1261   ATCCCCACAT GGACTGTGTC ATCACAGGAC GGCCCTGCTG CATTGGCACC AAGGGCAGGT

1321   GTGAGATCAC CTCCCGGGAG TACTGTGACT TCATGAGGGG CTACTTCCAT GAGGAGGCCA

1381   CGCTCTGCTC TCAGGTGCAC TGCATGGATG ATGTGTGTGG GCTCCTGCCT TTTCTCAACC

1441   CCGAGGTGCC TGACCAGTTC TACCGCCTGT GGCTATCCCT CTTCCTGCAC GCCGGGATCT

1501   TGCACTGCCT GGTGTCCATC TGCTTCCAGA TGACTGTCCT GCGGGACCTG GAGAAGCTGG

1561   CAGGCTGGCA CCGCATAGCC ATCATCTACC TGCTGAGTGG TGTCACCGGC AACCTGGCCA

1621   GTGCCATCTT CCTGCCATAC CGAGCAGAGG TGGGTCCCTGC TGGCTCCCAG TTCGGCATCC

1681   TGGCCCTGCCT CTTCGTGGAG CTCTTCCAGA GCTGGCAGAT CCTGGCGCGG CCCTGGGCGTG

1741   CCTTCTTCAA GCTGCTGGCT GTGGTGCTCT TCCTCTTCAC CTTTGGGCTG CTGCCGTGGA

1801   TTGACAACTT TGCCCACATC TCGGGGTTCA TCAGTGCCT CTTCCTCTCC TTCGCCTTCT

1861   TGCCCTACAT CAGCTTTGGC AAGTTCGACC TGTACCGGAA ACGCTGCCAG ATCATCATCT

1921   TTCAGGTGGT CTTCCTGGGC CTCCTGGCTG GCCTGGTGGT CCTCTTCTAC GTCTATCCTG

1981   TCCGGCTGTGA GTGGTGTGAG TTCCTCACCT GCATCCCCTT CACTGACAAG TTCTGTGAGA

2041   AGTACGAACT GGACGCTCAG TCCCACTGAG TCGACTCGAG CGGCCGCATC GTGACTGACT

2101   GACGATCTGC CTCGCGCGTT TCGGTGATGA CGGTGAAAAC CTCTGACACA TGCAGCTCCC

2161   GGAGACGGTC ACAGCTTGTC TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGCGC
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2221  GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACGTA GCGATAGCGG

2281  AGTGTATAAT TCTTGAAGAC GAAAGGGCCT CGTGATACGC CTATTTTTAT AGGTTAATGT

2341  CATGATAATA ATGGTTTCTT AGACGTCAGG TGGCACTTTT CGGGGAAATG TGCGCGGAAC

2401  CCCTATTTGT TTATTTTTCT AAATACATTC AAATATGTAT CCGCTCATGA GACAATAACC

2461  CTGATAAATG CTTCAATAAT ATTGAAAAAG GAAGAGTATG AGTATTCAAC ATTTCCGTGT

2521  CGCCCTTATT CCCTTTTTTG CGGCATTTTG CCTTCCTGTT TTTGCTCACC CAGAAACGCT

2581  GGTGAAAGTA AAAGATGCTG AAGATCAGTT GGGTGCACGA GTGGGTTACA TCGAACTGGA

2641  TCTCAACAGC GGTAAGATCC TTGAGAGTTT TCGCCCCGAA GAACGTTTTC CAATGATGAG

2701  CACTTTTAAA GTTCTGCTAT GTGGCGCGGT ATTATCCCGT GTTGACGCCG GGCAAGAGCA

2761  ACTCGGTCGC CGCATACACT ATTCTCAGAA TGACTTGGTT GAGTACTCAC CAGTCACAGA

2821  AAAGCATCTT ACGGATGGCA TGACAGTAAG AGAATTATGC AGTGCTGCCA TAACCATGAG

2881  TGATAACACT GCGGCCAACT TACTTCTGAC AACGATCGGA GGACCGAAGG AGCTAACCGC

2941  TTTTTTGCAC AACATGGGGG ATCATGTAAC TCGCCTTGAT CGTTGGGAAC CGGAGCTGAA

3001  TGAAGCCATA CCAAACGACG AGCGTGACAC CACGATGCCT GCAGCAATGG CAACAACGTT

3061  GCGCAAACTA TTAACTGGCG AACTACTTAC TCTAGCTTCC CGGCAACAAT TAATAGACTG

3121  GATGGAGGCG GATAAAGTTG CAGGACCACT TCTGCGCTCG GCCCTTCCGG CTGGCTGGTT

3181  TATTGCTGAT AAATCTGGAG CCGGTGAGCG TGGGTCTCGC GGTATCATTG CAGCACTGGG

3241  GCCAGATGGT AAGCCCTCCC GTATCGTAGT TATCTACACG ACGGGGAGTC AGGCAACTAT

3301  GGATGAACGA AATAGACAGA TCGCTGAGAT AGGTGCCTCA CTGATTAAGC ATTGGTAACT
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3361  GTCAGACCAA GTTTACTCAT ATATACTTTA GATTGATTTA AAACTTCATT TTTAATTTAA

3421  AAGGATCTAG GTGAAGATCC TTTTTGATAA TCTCATGACC AAAATCCCTT AACGTGAGTT

3481  TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA AAAGATCAAA GGATCTTCTT GAGATCCTTT

3541  TTTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAAACCA CCGCTACCAG CGGTGGTTTG

3601  TTTGCCGGAT CAAGAGCTAC CAACTCTTTT TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA

3661  GATACCAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTAGGC CACCACTTCA AGAACTCTGT

3721  AGCACCGCCT ACATACCTCG CTCTGCTAAT CCTGTTACCA GTGGCTGCTG CCAGTGGCGA

3781  TAAGTCGTGT CTTACCGGGT TGGACTCAAG ACGATAGTTA CCGGATAAGG CGCAGCGGTC

3841  GGGCTGAACG GGGGGTTCGT GCACACAGCC CAGCTTGGAG CGAACGACCT ACACCGAACT

3901  GAGATACCTA CAGCGTGAGC TATGAGAAAG CGCCACGCTT CCCGAAGGGA GAAAGGCGGA

3961  CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG

4021  AAACGCCTGG TATCTTTATA GTCCTGTCGG GTTTCGCCAC CTCTGACTTG AGCGTCGATT

4081  TTTGTGATGC TCGTCAGGGG GGCGGAGCCT ATGGAAAAAC GCCAGCAACG CGGCCTTTTT

4141  ACGGTTCCTG GCCTTTTGCT GGCCTTTTGC TCACATGTTC TTTCCTGCGT TATCCCCTGA

4201  TTCTGTGGAT AACCGTATTA CCGCCTTTGA GTGAGCTGAT ACCGCTCGCC GCAGCCGAAC

4261  GACCGAGCGC AGCGAGTCAG TGAGCGAGGA AGCGGAAGAG CGCCCGATGC GGTATTTTCT

4321  CCTTACGCAT CTGTGCGGTA TTTCACACCG CATAAATTCC GACACCATCG AATGGTGCAA

4381  AACCTTTCGC GGTATGGCAT GATAGCGCCC GGAAGAGAGT CAATTCAGGG TGGTGAATGT

4441  GAAACCAGTA ACGTTATACG ATGTCGCAGA GTATGCCGGT GTCTCTTATC AGACCGTTTC
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4501  CCGCGTGGTG  AACCAGGCCA  GCCACGTTTC  TGCGAAAACG  CGGGAAAAAG  TGGAAGCGGC

4561  GATGGCGGAG  CTGAATTACA  TTCCCAACCG  CGTGGCACAA  CAACTGGCGG  GCAAACAGTC

4621  GTTGCTGATT  GGCGTTGCCA  CCTCCAGTCT  GGCCCTGCAC  GCGCCGTCGC  AAATTGTCGC

4681  GGCGATTAAA  TCTCGCGCCG  ATCAACTGGG  TGCCAGCGTG  GTGGTGTCGA  TGGTAGAACG

4741  AAGCGGCGTC  GAAGCCTGTA  AAGCGGCGGT  GCACAATCTT  CTCGCGCAAC  GCGTCAGTGG

4801  GCTGATCATT  AACTATCCGC  TGGATGACCA  GGATGCCATT  GCTGTGGAAG  CTGCCTGCAC

4861  TAATGTTCCG  GCGTTATTTC  TTGATGTCTC  TGACCAGACA  CCCATCAACA  GTATTATTTT

4921  CTCCCATGAA  GACGGGTACGC GACTGGGCGT  GGAGCATCTG  GTCGCATTGG  GTCACCAGCA

4981  AATCGCGCTG  TTAGCGGGCC  CATTAAGTTC  TGTCTCGGCG  CGTCTGCGTC  TGGCTGGCTG

5041  GCATAAATAT  CTCACTCGCA  ATCAAATTCA  GCCGATAGCG  GAACGGGAAG  GCGACTGGAG

5101  TGCCATGTCC  GGTTTTCAAC  AAACCATGCA  AATGCTGAAT  GAGGGCATCG  TTCCCACTGC

5161  GATGCTGGTT  GCCAACGATC  AGATGGCGCT  GGGCGCAATG  CGGCGCCATTA CCGAGTCCGG

5221  GCTGCGCGTT  GGTGCGGATA  TCTCGGTAGT  GGGATACGCA  GATACCGAAG  ACAGCTCATG

5281  TTATATCCCG  CCGTTAACCA  CCATCAAACA  GGATTTTCGC  CTGCTGGGGC  AAACCAGCGT

5341  GGACCGCTTG  CTGCAACTCT  CTCAGGGCCA  GGCGGTGAAG  GGCAATCAGC  TGTTGCCCGT

5401  CTCACTGGTG  AAAAGAAAAA  CCACCCTGGC  GCCCAATACG  CAAACCGCCT  CTCCCCGCGC

5461  GTTGGCCGAT  TCATTAATGC  AGCTGGCACG  ACAGGTTTCC  CGACTGGAAA  GCGGGCAGTG

5521  AGCGCAACGC  AATTAATGTG  AGTTAGCTCA  CTCATTAGGC  ACCCCAGGCT  TTACACTTTA

5581  TGCTTCCGGC  TCGTATGTTG  TGTGGAATTG  TGAGCGGATA  ACAATTTCAC  ACAGGAAACA
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5641 GCTATGACCA TGATTACGGA TTCACTGGCC GTCGTTTTAC AACGTCGTGA CTGGGAAAAC
5701 CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG CTGGCGTAAT
5761 AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA TGGCGAATGG
5821 CGCTTTGCCT GGTTTCCGGC ACCAGAAGCG GTGCCGGAAA GCTGGCTGGA GTGCGATCTT
5881 CCTGAGGCCG ATACTGTCGT CGTCCCCTCA AACTGGCAGA TGCACGGTTA CGATGCGCCC
5941 ATCTACACCA ACGTAACCTA TCCCATTACG GTCAATCCGC CGTTTGTTCC CACGGAGAAT
6001 CCGACGGGTT GTTACTCGCT CACATTTAAT GTTGATGAAA GCTGGCTACA GGAAGGCCAG
6061 ACGCGAATTA TTTTTGATGG CGTTGGAATT
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FIG. 30, (SEQ ID NO:66) ICT1024 coding region: 310-2879

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   1  TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT
  61  TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG GGCCTCTTCG
 121  CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGTAACGCCA
 181  GGGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG ATTGGCTAGC
 241  AGAATAAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGGAGCTCGT
 301  GGATCCGAAT TCCATGAGTG AGGCCCGCAG GGACAGCACG AGCAGCCTGC AGCGCAAGAA
 361  GCCACCCTGG CTAAAGCTGG ACATTCCCTC TGCGGTGCCC CTGACGGGCAG AAGAGCCCAG
 421  CTTCCTGCAG CCCCTGAGGC GACAGGCTTT CCTGAGGAGT GTGAGTATGC CAGCCGAGAC
 481  AGCCCACATC TCTTCACCCC ACCATGAGCT CCGGCGGCCG GTGCTGCAAC GCCAGACGTC
 541  CATCACACAG ACCATCCGCA GGGGGACCGC CGACTGGTTT GGAGTGAGCA AGGACAGTGA
 601  CAGCACCCAG AAATGGCAGC GCAAGAGCAT CCGTCACTGC AGCCAGCGCT ACGGGAAGCT
 661  GAAGCCCCAG GTCCTCCGGG AGCTGGACCT GCCCAGCCAG GACAACGTGT CGCTGACCAG
 721  CACCGAGACG GCCCGTGGCC TCTACGTGGG GTGCCTTCCG GCCATGCCAG AGAAGATCAT
 781  AGACCCCCTG GCCCGGGCTC CGCCGGGTGC TGTGGCAGAT GACACTGCGG AAGGCCTGAG
 841  TGCCCCACAC ACTCCCGTCA CGCCGGGCTCC CGCGGCGGCG TGCCTCCCTC CCAGCTCCCG
 901  CTCAGGTTTC CACCGGCTCC CGCGGCGGCG CAAGCGAGAG TCGGTGGCCA AGATGAGCTT
 961  CCGGGCGGCC GCAGCGCTGA TGAAAGGCCCG CTCCGTTAGG GATGGCACCT TTCGCCGGGC
1021  ACGGGCGTCGA AGCTTCACTC CAGCTAGCTT TCTGGAGGAG GACACAACTG ATTCCCCGA
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1081   TGAGCTGGAC ACATCCTTCT TTGCCCGGGA AGGTATCCTC CATGAAGAGC TGTCCACATA
1141   CCCGGATGAA GTTTTCGAGT CCCCATCGGA GGCAGCGCTA AAGGACTGGG AGAAGGCACC
1201   GGAGCAGGCG GACCTCACCG GCGGGGGCCCT GGACCGCAGC GAGCTTGAGC GCAGCCACCT
1261   GATGCTGCCC TTGGAGCGAG GCTGGCGGAA GCAGAAGGAG GGGCCCGGCAG CCCCGCAGCC
1321   CAAGGTGCGG CTCCGACAGG AGGTGGTGAG CACCGCGGGG CCGCGACGGG GCCAGCGTAT
1381   CGCGGTGCCG GTGCGCGAAGC TCTTCGCCCG GGAGAAGCGG CCGTATGGGC TGGGCATGGT
1441   GGGACGGCTC ACCAACCGCA CCTACCGCAA GCGCATCGAC AGCTTCGTCA AGCGCCAGAT
1501   CGAGGACATG GACGACCACA GGCCCTTCTT CACCTACTGG CTTACCTTCG TGCACTCGCT
1561   CGTCACCATC CTAGCCGTGT GCATCTATGG CATCGCGCCC GTGGGCTTCT CGCAGCATGA
1621   GACGGTGGAC TCGGTGCTGC GGAACCGCGG GGTCTACGAG AACGTCAAGT ACGTGCAGCA
1681   GGAGAACTTC TGGATCGGGC CCAGCTCGGA GGCCCTCATC CACCTGGGCG CCAAGTTTTC
1741   GCCCTGCATG CGCCAGGACC CGCAGGTGCA CAGCTTCATT CGCTCGGCGC GCGAGCGCGA
1801   GAAGCACTCC GCCTGCTGCG TGGCCAACGA CAGGTCGGGC TGCGTGCAGA CCTCGGAGGA
1861   GGAGTGCTCG TCCACGCTGG CAGTGTGGGT GAAGTGGCCC ATCCATCCCA GCGCCCCAGA
1921   GCTTGCGGGC CACAAGAGAC AGTTTGGCTC TGTCTGCCAC CAGGATCCCA GGGTGTGTGA
1981   TGAGCCCTCC TCCGAAGACC CTCATGAGTG GCCAGAGAGAC ATCACCAAGT GGCCGATCTG
2041   CACCAAAAAC AGCGCTGGGA ACCACACCAA CCATCCCCAC ATGGACTGTG TCATCACAGG
2101   ACGGCCCCTGC TGCATTGGCA CCAAGGGGCAG GTGTGAGATC ACCTCCCGGG AGTACTGTGA
2161   CTTCATGAGG GGCTACTTCC ATGAGGAGGC CACGCTCTGC TCTCAGGTGC ACTGCATGGA
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2221  TGATGTGTGT  GGGCTCCTGC  CTTTTCTCAA  CCCCGAGGTG  CCTGACCAGT  TCTACCGCCT
2281  GTGGCTATCC  CTCTTCCTGC  ACGCCGGGAT  CTTGCACTGC  CTGGTGTCCA  TCTGCTTCCA
2341  GATGACTGTC  CTGCGGGACC  TGGAGAAGCT  GGCAGGCTGG  CACCGCATAG  CCATCATCTA
2401  CCTGCTGAGT  GGTGTCACCG  GCAACCTGGC  CAGTGCCATC  TTCCTGCCAT  ACCGAGCAGA
2461  GGTGGGTCCT  GCTGGCTCCC  AGTTCGGCAT  CCTGGCCTGC  CTCTTCGTGG  AGCTCTTCCA
2521  GAGCTGGCAG  ATCCTGGCGC  GGCCCTGGCG  TGCCTTCTTC  AAGCTGCTGG  CTGTGGTGCT
2581  CTTCCTCTTC  ACCTTTGGGC  TGCTGCCGTG  GATTGACAAC  TTTGCCCACA  TCTCGGGGTT
2641  CATCAGTGGC  CTCTTCCTCT  CCTTGCCCTT  CTTGCCCTAC  ATCAGCTTTG  GCAAGTTCGA
2701  CCTGTACCGG  AAACGCTGCC  AGATCATCAT  CTTTCAGGTG  GTCTTCCTGG  GCCTCCTGGC
2761  TGGCCTGGTG  GTCCTCTTCT  ACGTCTATCC  TGTCCGCTGT  GAGTGGTGTG  AGTTCCTCAC
2821  CTGCATCCCC  TTCACTGACA  AGTTCTGTGA  GAAGTACGAA  CTGGACGCTC  AGCTCCACAT
2881  CGATACGCGT  TCGAAGCTTG  CGGCCGCACA  GCTGTATACA  CGTGCAAGCC  AGCCAGAACT
2941  CGCTCCTGAA  GACCCAGAGG  ATCTCGAGCA  CCACCACCAC  CACCACTAAT  GTTAATTAAG
3001  TTGGGGCGTTG TAATCATAGT  CATAATCAAT  ACTCCTGACT  GCGTTAGCAA  TTTAACTGTG
3061  ATAAACTACC  GCATTAAAGC  TATTCGATGA  TAAGCTGTCA  AACATGATAA  TTCTTGAAGA
3121  CGAAAGGGCC  TAGGCTGATA  AAACAGAATT  TGCCTGGCGG  CAGTAGCGCG  GTGGTCCCAC
3181  CTGACCCCAT  GCCGAACTCA  GAAGTGAAAC  GCCGTAGCGC  CGATGGTAGT  GTGGGGTCTC
3241  CCCATGCGAG  AGTAGGGAAC  TGCCAGGCAT  CAAATAAAAC  GAAAGGCTCA  GTCGAAAGAC
3301  TGGGCCTTTC  GTTTTATCTG  TTGTTTGTCG  GTGAACGCTC  TCCTGAGTAG  GACAAATCCG
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3361  CCGGGAGCGG ATTTGAACGT TGCGAAGCAA CGGCCCGGAG GGTGGCGGGC AGGACGCCCG

3421  CCATAAACTG CCAGGCATCA AATTAAGCAG AAGGCCATCC TGACGGATGG CCTTTTTGCG

3481  TTTCTACAAA CTCTTTTGTT TATTTTTCTA AATACATTCA AATATGTATC CGCTGAGCAA

3541  TAACTAGCAT AACCCCTTGG GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA

3601  GGAACTATAT CCGGATTGGC GAATGGGACG CGCCCTGTAG CGGCGCATTA AGCGCGGCGG

3661  GTGTGGTGGT TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCCGCTCCTT

3721  TCGCTTTCTT CCCTTCCTTT CTCGCCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAAATC

3781  GGGGGCTCCC TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC AAAAAACTTG

3841  ATTAGGGTGA TGGTTCACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCCTTTGA

3901  CGTTGGAGTC CACGTTCTTT AATAGTGGAC TCTTGTTCCA AACTGGAACA ACACTCAACC

3961  CTATCTCGGT CTATTCTTTT GATTTATAAG GGATTTTGCC GATTTCGGCC TATTGGTTAA

4021  AAAAATGAGCT GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA ACGTTTACAA

4081  TTTCTGGCGG CACGATGGCA TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA

4141  TTAAAAATGA AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA

4201  CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT CATCCATAGT

4261  TGCCTGACTC CCCGTCGTGT AGATAACTAC GGCTTACCAT CTGGCCCCAG

4321  TGCTGCAATG ATACCGCGAG ACCCACGCTC ACCGGCTCCA GATTTATCAG CAATAAACCA

4381  GCCAGCCGGA AGGGCCGAGC GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC

4441  TATTAATTGT TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT
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4501  TGTTGCCATT GCTACAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG
4561  CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT
4621  TAGCTCCTTC GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG GCCGCAGTGT TATCACTCAT
4681  GGTTATGGCA GCACTGCATA ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT
4741  GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC
4801  TTGCCCGGCG TCAATACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT
4861  CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC TTACCGCTGT TGAGATCCAG
4921  TTCGATGTAA CCCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT
4981  TTCTGGGTGA GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG
5041  GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATCATGA CCAAAATCCC TTAACGTGAG
5101  TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT
5161  TTTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT
5221  TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG
5281  CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT
5341  GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC
5401  GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG
5461  TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA
5521  CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG
5581  GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG
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5641   GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA

5701   TTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT

5761   TTACGGTTCC TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT

5821   GATTCTGTGG ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA

5881   ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCCGGCG ATAATGGCCT GCTTCTCGCC

5941   GAAACGTTTG GTGGCGGGAC CAGTGACGAA GGGGCGGTGCA AGATTCCGAA

6001   TACCGCAAGC GACAGGCCGA TCATCGTCGC GCTCCAGCGA AAGCGGTCCT CGCCGAAAAT

6061   GACCCAGAGC GCTGCCGGCA CCTGTCCTAC GAGTTGCATG ATAAAGAAGA CAGTCATAAG

6121   TGCGGCGACG ACCGGTGAAT TGTGAGCGCT CACAATTCTC GTGACATCAT AACGTCCCGC

6181   GAAAT
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FIG. 31, (SEQ ID NO:68) Coding region for the N terminus 400 aa of ICT1024: 314-1515

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   1  TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT
  61  TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG GGCCTCTTCG
 121  CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGTAACGCCA
 181  GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG ATTGGCTAGC
 241  AGAATAATTT TGTTTAAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGGAGCTCGT
 301  GGATCCGAAT TCCATGAGTG AGGCCCGCAG GGACAGCACG AGCAGCCTGC AGCGCAAGAA
 361  GCCACCCTGG CTAAAGCTGG ACATTCCCTC TGCGGTGCCC CTGACGGCAG AAGAGCCCAG
 421  CTTCCTGCAG CCCCTGAGGC GACAGGCTTT CCTGAGGAGT GTGAGTATGC CAGCCGAGAC
 481  AGCCCACATC TCTTCACCCC ACCATGAGCT CCGGCGGCCG GTGCTGCAAC GCCAGACGTC
 541  CATCACACAG ACCATCCCGCA GGGGGACCGC CGACTGGTTT GGAGTGAGCA AGGACAGTGA
 601  CAGCACCCAG AAATGGCAGC GCAAGAGCAT CCGTCACTGC AGCCAGCGCT ACGGGAAGCT
 661  GAAGCCCCAG GTCCTCCGGG AGCTGGACCT GCCCAGCCAG GACAACGTGT CGCTGACCAG
 721  CACCGAGACG CCACCCCCAC TCTACGTGGG GCCATGCCAG CTGGGCATGC AGAAGATCAT
 781  AGACCCCCTG GCCCGTGGCC GTGCCTTCCG TGTGGCAGAT GACACTGCGG AAGGCCTGAG
 841  TGCCCCACAC ACTCCCGTCA CGCCGGGTGC TGCCTCCCTC TGCTCCTTCT CCAGCTCCCG
 901  CTCAGGTTTC CACCGGCTCC CGCGGCGGCG CAAGCGAGAG TCGGTGGCCA AGATGAGCTT
 961  CCGGGGGGCC GCAGCGGCTGA TGAAAGGCCG CTCCGTTAGG GATGGCACCT TTCGCGGGGC
1021  ACGGCGTCGA AGCTTCACTC CAGCTAGCTT TCTGGAGGAG GACACAACTG ATTTCCCGA
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1081  TGAGCTGGAC ACATCCTTCT TTGCCCGGGA AGGTATCCTC CATGAAGAGC TGTCCACATA
1141  CCCGGATGAA GTTTTCGAGT CCCCATCGGA GGCAGCGCTA AAGGACTGGG AGAAGGCACC
1201  GGAGCAGGCG GACCTCACCG GCGGGGCCCT GGACCGCAGC GAGCTTGAGC GCAGCCACCT
1261  GATGCTGCCC TTGGAGCGAG GCTGGCGGAA GCAGAAGGAG GGCGCCGCAG CCCCGCAGCC
1321  CAAGGTGCGG CTCCGACAGG AGGTGGTGAG CACCGCGGGG CCGGACGGG GCCAGCGTAT
1381  CGCGGTGCCG GTGCGCAAGC TCTTCGCCCG GGAGAAGCGG CCGTATGGGC TGGGCATGGT
1441  GGGACGGCTC ACCAACCGCA CCTACCGCAA GCGCCATCGAC AGCTTCGTCA AGCGCCAGAT
1501  CGAGGACATG GACATCGATA CGCGTTCGAA GCTTGCGGCC GCACAGCTGT ATACACGTGC
1561  AAGCCAGCCA GAACTCGCTC CTGAAGACCC AGAGGATCTC GAGCACCACC ACCACCACCA
1621  CTAATGTTAA TTAAGTTGGG CGTTGTAATC ATAGTCATAA TCAATACTCC TGACTGCGTT
1681  AGCAATTTAA CTGTGATAAA CTACCGCATT AAAGCTATTC GATGATAAGC TGTCAAACAT
1741  GATAATTCTT GAAGACGAAA GGGCCTAGGC TGATAAAACA GAATTTGCCT GGCGGCAGTA
1801  GCGCGGTGGT CCCACCTGAC CCCATGCCGA ACTCAGAAGT GAAACGCCGT AGCGCCGATG
1861  GTAGTGTGGG GTCTCCCCAT GCGAGAGTAG GGAACTGCCA GGCATCAAAT AAAACGAAAG
1921  GCTCAGTCGA AAGACTGGGC CTTTCGTTTT ATCTGTTGTT TGTCGGTGAA CGCTCTCCTG
1981  AGTAGGACAA ATCCGCCGGG AGCGGATTTG AACGTTGCGA AGCAACGGCC CGGAGGGTGG
2041  CGGGCAGGAC GCCCGCCATA AACTGCCAGG CATCAAATTA AGCAGAAGGC CATCCTGACG
2101  GATGGCCTTT TTGCCGTTTCT ACAAACTCTT TTGTTTATTT TTCTAAATAC ATTCAAATAT
2161  GTATCCGCTG AGCAATAACT AGCATAACCC CTTGGGGCCT CTAAACGGGT CTTGAGGGGT
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2221  TTTTTGCTGA AAGGAGGAAC TATATCCGGA TTGGCGAATG GGACGCGCCC TGTAGCGGCG
2281  CATTAAGCGC GGCGGGGTGTG GTGGTTACGC GCAGCGTGAC CGCTACACTT GCCAGCGCCC
2341  TAGCGCCCGC TCCTTTCGCT TTCTTCCCTT CCTTTCTCGC CACGTTCGCC GGCTTTCCCC
2401  GTCAAGCTCT AAATCGGGGG CTCCCTTTAG GGTTCCGATT TAGTGCTTTA CGGCACCTCG
2461  ACCCCAAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC TGATAGACGG
2521  TTTTTCGCCC TTTGACGTTG GAGTCCACGT TCTTTAATAG TGGACTCTTG TTCCAAACTG
2581  GAACAACACT CAACCCTATC TCGGTCTATT CTTTTGATTT ATAAGGGATT TTGCCGATTT
2641  CGGCCTATTG GTTAAAAAAT GAGCTGATTT AACAAAAATT TAACGCGAAT TTTAACAAAA
2701  TATTAACGTT TACAATTTCT GGCGGCACGA TGGCATGAGA TTATCAAAAA GGATCTTCAC
2761  CTAGATCCTT TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC
2821  TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT
2881  TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT
2941  ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCCAGATTT
3001  ATCAGCAATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC
3061  CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA
3121  TAGTTTGCGC AACGTTGTTG CCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTTGG
3181  TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT
3241  GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC
3301  AGTGTTATCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT
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3361   AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG

3421   GCGACCGAGT TGCTCTTGCC CGGCGTCAAT ACGGGATAAT ACCGCGCCAC ATAGCAGAAC

3481   TTTAAAAGTG CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACTCTCAA GGATCTTACC

3541   GCTGTTGAGA TCCAGTTCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT

3601   TACTTTCACC AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG

3661   AATAAGGGCG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT CATGACCAAA

3721   ATCCCTTAAC GTGAGTTTTC GTTCCACTGA GCGTCAGACC CCGTAGAAAA GATCAAAGGA

3781   TCTTCTTGAG ATCCTTTTTT TCTGCGCGTA ATCTGCTGCT TGCAAACAAA AAAACCACCG

3841   CTACCAGCGG TGGTTTGTTT GCCGGATCAA GAGCTACCAA CTCTTTTTCC GAAGGTAACT

3901   GGCTTCAGCA GAGCGCAGAT ACCAAATACT GTCCTTCTAG TGTAGCCGTA GTTAGGCCAC

3961   CACTTCAAGA ACTCTGTAGC ACCGCCTACA TACCTCGCTC TGCTAATCCT GTTACCAGTG

4021   GCTGCTGCCA GTGGCGATAA GTCGTGTCTT ACCGGGTTGG ACTCAAGACG ATAGTTACCG

4081   GATAAGGCGC AGCGGTCGGG CTGAACGGGG GGTTCGTGCA CACAGCCCAG CTTGGAGCGA

4141   ACGACCTACA CCGAACTGAG ATACCTACAG CGTGAGCTAT GAGAAAGCGC CACGCTTCCC

4201   GAAGGGAGAA AGGCGGACAG GTATCCGGTA AGCGGCAGGG TCGGAACAGG AGAGCGCACG

4261   AGGGAGCTTC CAGGGGGAAA CGCCTGGTAT CTTTATAGTC CTGTCGGGTT TCGCCACCTC

4321   TGACTTGAGC GTCGATTTTT GTGATGCTCG TCAGGGGGGC GGAGCCTATG GAAAAACGCC

4381   AGCAACGCGG CCTTTTTACG GTTCCTGGCC TTTTGCTGGC CTTTTGCTCA CATGTTCTTT

4441   CCTGCGTTAT CCCCTGATTC TGTGGATAAC CGTATTACCG CCTTTGAGTG AGCTGATACC
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4501  GCTCGCCGCA GCCGAACGAC CGAGCGCAGC GAGTCAGTGA GCGAGGAAGC CGGCGATAAT

4561  GGCCTGCTTC TCGCCGAAAC GTTTGGTGGC GGGACCAGTG ACGAAGGCTT GAGCGAGGGC

4621  GTGCAAGATT CCGAATACCG CAAGCGACAG GCCGATCATC GTCGCGCTCC AGCGAAAGCG

4681  GTCCTCGCCG AAAATGACCC AGAGCGCTGC CGGCACCTGT CCTACGAGTT GCATGATAAA

4741  GAAGACAGTC ATAAGTGCGG CGACGACCGG TGAATTGTGA GCGGCTCACAA TTCTCGTGAC

4801  ATCATAACGT CCCGGCGAAAT
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FIG. 32, (SEQ ID NO 69) Coding region for the C terminus 373 aa of ICT1024: 308-1431

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   1  TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT

  61  TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG GGCCTCTTCG

 121  CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGTAACGCCA

 181  GGGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG ATTGGCTAGC

 241  AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGGAGCTCGT

 301  GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG AGAAGCACTC

 361  CGCCTGCTGC GTGCGCAACG ACAGGTCGGG CTGCGTGCAG ACCTCGGAGG AGGAGTGCTC

 421  GTCCACGCTG GCAGTGTGGG TGAAGTGGCC CATCCATCCC AGCGCCCCAG AGCTTGCGGG

 481  CCACAAGAGA CAGTTTGGCT CTGTCTGCCA CCAGGATCCC AGGGTGTGTG ATGAGCCCTC

 541  CTCCGAAGAC CCTCATGAGT GGCCAGAGA CATCACCAAG TGGCCCGATCT GCACCAAAAA

 601  CAGCGGCTGGG AACCACACCA ACCATCCCCA CATGGACTGT GTCATCACAG GACGGCCCTG

 661  CTGCATTGGC ACCAAGGGCA GGTGTGAGAT CACCTCCCGG GAGTACTGTG ACTTCATGAG

 721  GGGCTACTTC CATGAGGAGG CCACGCTCTG CTCTCAGGTG CACTGGCATGG ATGATGTGTG

 781  TGGGCTCCTG CCTTTTCTCA ACCCCGAGGT GCCTGACCAG TTCTACCGCC TGTGGCTATC

 841  CCTCTTCCTG CACGCCGGGA TCTTGCACTG CCTGGTGTCC ATCTGCTTCC AGATGACTGT

 901  CCTGCGGGAC CTGGAGAAGC TGGCAGGCTG GCACCGGCATA GCCATCATCT ACCTGCTGAG

 961  TGGTGTCACC GGCAACCTGG CCAGTGCCAT CTTCCTGCCA TACCGAGCAG AGGTGGGTCC

1021  TGCTGGCTCC CAGTTCGGCA TCCTGGCCTG CCTCTTCGTG GAGCTCTTCC AGAGCTGGCA
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1081   GATCCTGGCG CGGCCCTGGC GTGCCTTCTT CAAGCTGCTG GCTGTGGTGC TCTTCCTCTT
1141   CACCTTTGGG CTGCTGCCGT GGATTGACAA CTTTGCCCAC ATCTCGGGGT TCATCAGTGG
1201   CCTCTTCCTC TCCTTCGCCT TCTTGCCCTA CATCAGCTTT GGCAAGTTCG ACCTGTACCG
1261   GAAACGCTGC CAGATCATCA TCTTTCAGGT GGTCTTCCTG GGCCTCCTGG CTGGCCTGGT
1321   GGTCCTCTTC TACGTCTATC CTGTCCGCTG TGAGTGGTGT GAGTTCCTCA CCTGCATCCC
1381   CTTCACTGAC AAGTTCTGTG AGAAGTACGA ACTGGACGCT CAGCTCCACA TCGATACGCG
1441   TTCGAAGCTT GCGGCCGCAC AGCTGTATAC ACGTGCAAGC CAGCCAGAAC TCGCTCCTGA
1501   AGACCCAGAG GATCTCGAGC ACCACCACCA CCACCACTAA TGTTAATTAA GTTGGGCGTT
1561   GTAATCATAG TCATAATCAA TACTCCTGAC TGCGTTAGCA ATTTAACTGT GATAAACTAC
1621   CGCATTAAAG CTATTCGATG ATAAGCTGTC AAACATGATA ATTCTTGAAG ACGAAAGGGC
1681   CTAGGCTGAT AAAACAGAAT TTGCCTGGCG GCAGTAGCGC GGTGGTCCCA CCTGACCCCA
1741   TGCCGAACTC AGAAGTGAAA CGCCGTAGCG CCGATGGTAG TGTGGGGTCT CCCCATGCGA
1801   GAGTAGGGAA CTGCCAGGCA TCAAATAAAA CGAAAGGCTC AGTCGAAAGA CTGGGCCTTT
1861   CGTTTTATCT GTTGTTTGTC GGTGAACGCT CTCCTGAGTA GGACAAATCC GCCGGGAGCG
1921   GATTTGAACG TTGCGAAGCA ACGGCCCGGA GGGTGGCGGG CAGGACGCCC GCCATAAACT
1981   GCCAGGCATC AAATTAAGCA GAAGGCCATC CTGACGGATG GCCTTTTTGC GTTTCTACAA
2041   ACTCTTTTGT TTATTTTTCT AAATACATTC AAATATGTAT CCGCTGAGCA ATAACTAGCA
2101   TAACCCCTTG GGGCCTCTAA ACGGGTCTTG AGGGGTTTTT TGCTGAAAGG AGGAACTATA
2161   TCCGGATTGG CGAATGGGAC GCGCCCTGTA GCGGCGCATT AAGCGCGGCG GGTGTGGTGG
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2221   TTACGCGCAG   CGTGACCGCT   ACACTTGCCA   GCGCCCTAGC   GCCCGCTCCT   TTCGCTTTCT
2281   TCCCTTCCTT   TCTCGCCACG   TTCGCCGGCT   TTCCCCGTCA   AGCTCTAAAT   CGGGGGCTCC
2341   CTTTAGGGTT   CCGATTTAGT   GCTTTACGGC   ACCTCGACCC   CAAAAAACTT   GATTAGGGTG
2401   ATGGTTCACG   TAGTGGGCCA   TCGCCCTGAT   AGACGGTTTT   TCGCCCTTTG   ACGTTGGAGT
2461   CCACGTTCTT   TAATAGTGGA   CTCTTGTTCC   AAACTGGAAC   AACACTCAAC   CCTATCTCGG
2521   TCTATTCTTT   TGATTTATAA   GGGATTTTGC   CGATTTCGGC   CTATTGGTTA   AAAAATGAGC
2581   TGATTTAACA   AAAATTTAAC   GCGGAATTTTA   ACAAAAATATT   AACGTTTACA   ATTTCTGGCG
2641   GCACGATGGC   ATGAGATTAT   CAAAAAGGAT   CTTCACCTAG   ATCCTTTTAA   ATTAAAAATG
2701   AAGTTTTAAA   TCAATCTAAA   GTATATATGA   GTAAACTTGG   TCTGACAGTT   ACCAATGCTT
2761   AATCAGTGAG   GCACCTATCT   CAGCGATCTG   TCTATTTCGT   TCATCCATAG   TTGCCTGACT
2821   CCCCGTCGTG   TAGATAACTA   CGATACGGGA   GGGCTTACCA   TCTGGCCCCA   GTGCTGCAAT
2881   GATACCGCGA   GACCCACGCT   CACCGGCTCC   AGATTTATCA   GCAATAAACC   AGCCAGCCGG
2941   AAGGGCCGAG   CGCAGAAGTG   GTCCTGCAAC   TTTATCCGCC   TCCATCCAGT   CTATTAATTG
3001   TTGCCGGGAA   GCTAGAGTAA   GTAGTTCGCC   AGTTAATAGT   TTGCGCAACG   TTGTTGCCAT
3061   TGCTACAGGC   ATCGTGGTGT   CACGCTCGTC   GTTTGGTATG   GCTTCATTCA   GCTCCGGTTC
3121   CCAACGATCA   AGGCGAGTTA   CATGATCCCC   CATGTTGTGC   AAAAAAGCGG   TTAGCTCCTT
3181   CGGTCCTCCG   ATCGTTGTCA   GAAGTAAGTT   GGCCGCAGTG   TTATCACTCA   TGGTTATGGC
3241   AGCACTGCAT   AATTCTCTTA   CTGTCATGCC   ATCCGTAAGA   TGCTTTTCTG   TGACTGGTGA
3301   GTACTCAACC   AAGTCATTCT   GAGAATAGTG   TATGCGGCGA   CCGAGTTGCT   CTTGCCCGGC
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3361  GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA

3421  ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA

3481  ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG

3541  AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG

3601  AATACTCATA CTCTTCCTTT TTCAATCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC

3661  CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTCTG

3721  CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG

3781  GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATACCA

3841  AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG

3901  CCTACATACC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG

3961  TGTCTTACCG GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA

4021  ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC

4081  CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT

4141  CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC

4201  TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA

4261  TGCTCGTCAG GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC

4321  CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG

4381  GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG

4441  CGCAGCGAGT CAGTGAGCGA GGAAGCCGGC GATAATGCC TGCTTCTCGC CGAAACGTTT
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4501  GGTGGCGGGA CCAGTGACGA AGGCTTGAGC GAGGGCGTGC AAGATTCCGA ATACCGCAAG

4561  CGACAGGCCG ATCATCGTCG CGCTCCAGCG AAAGCGGTCC TCGCCGAAAA TGACCCAGAG

4621  CGCTGCCGGC ACCTGTCCTA CGAGTTGCAT GATAAAGAAG ACAGTCATAA GTGCGGCGAC

4681  GACCGGTGAA TTGTGAGCGC TCACAATTCT CGTGACATCA TAACGTCCCG CGAAAT
```

Figure 52. HLA peptide motif search results

User Parameters and Scoring Information	
method selected to limit number of results	explicit number
number of results requested	20
HLA molecule type selected	A_0201
length selected for subsequences to be scored	9
echoing mode selected for input sequence	Y
echoing format	numbered lines
length of user's input peptide sequence	803
number of subsequence scores calculated	795
number of top-scoring subsequences reported back in scoring output table	20

Scoring Results			
Rank	Start Position	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1	425	MMPKYLNFV	1080.239
2	410	KLYVRRVFI	642.660
3	557	RLLKKGYEV	257.342
4	203	FLVADKVIV	131.175
5	144	LLHVTDTGV	118.238
6	547	KEAESSPFV	106.738
7	639	RLTESPCAL	87.586
8	381	VTFKSILFV	76.863
9	3	ALWVLGLCC	41.234
10	6	VLGLCCVLL	36.316
11	189	SELIGQFGV	29.023
12	741	RMLRLSLNI	27.879
13	451	LQQHKLLKV	27.573
14	280	YVWSSKTET	24.895
15	259	LELDTIKNL	24.638
16	417	FITDDFHDM	24.478
17	467	KTLDMIKKI	17.695
18	463	KLVRKTLDM	17.388

19	429	YLNFVKGVV	17.053
20	197	VGFYSAFLV	16.564

Figure 53. Suggested models for transmembrane topology for ICT1025

-----> STRONGLY prefered model: N-terminus inside
2 strong transmembrane helices, total score : 2962
from   to length score orientation
1   3   19 (17)   2034 i-o
2 191 212 (22)   928 o-i

------> alternative model
2 strong transmembrane helices, total score : 2607
from   to length score orientation
1   3   19 (17)   1929 o-i
2 191 213 (23)   678 i-o

Figure 54.."DAS" - Transmembrane Prediction server ICT 1025

Potential transmembrane segments

Start	Stop	Length	~	Cutoff
6	18	13	~	1.7*
7	17	11	~	2.2
195	209	15	~	1.7*
197	206	10	~	2.2
247	248	2	~	1.7
384	390	7	~	1.7
710	723	14	~	1.7
713	719	7	~	2.2*

Living Cell surface ELISA for screening 1025-antibody containing supernatants in MDA-MB-435 cells
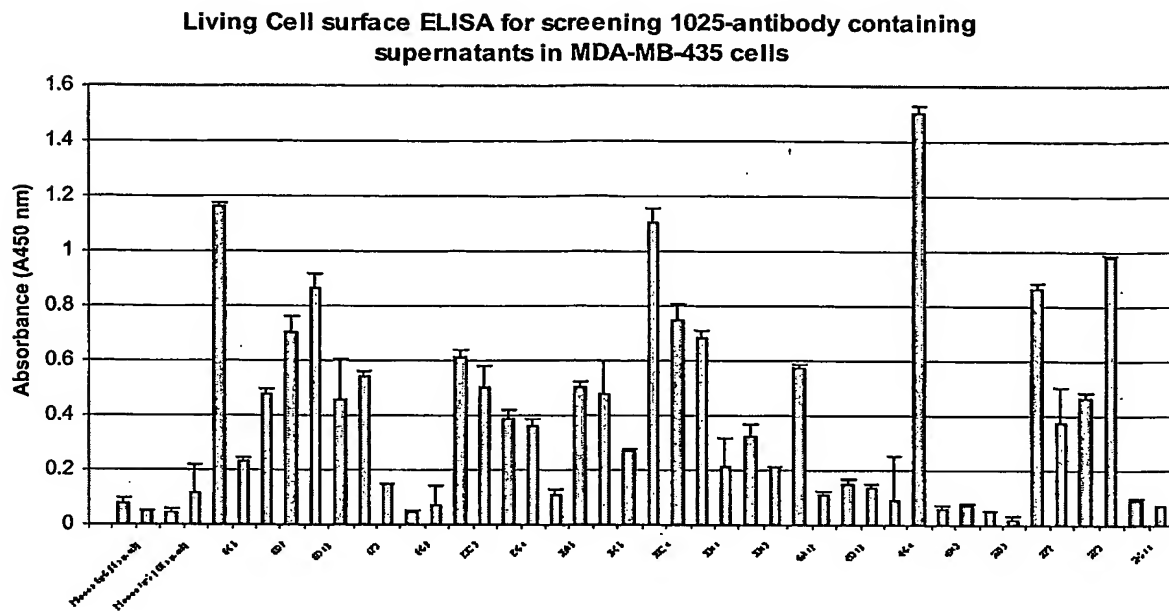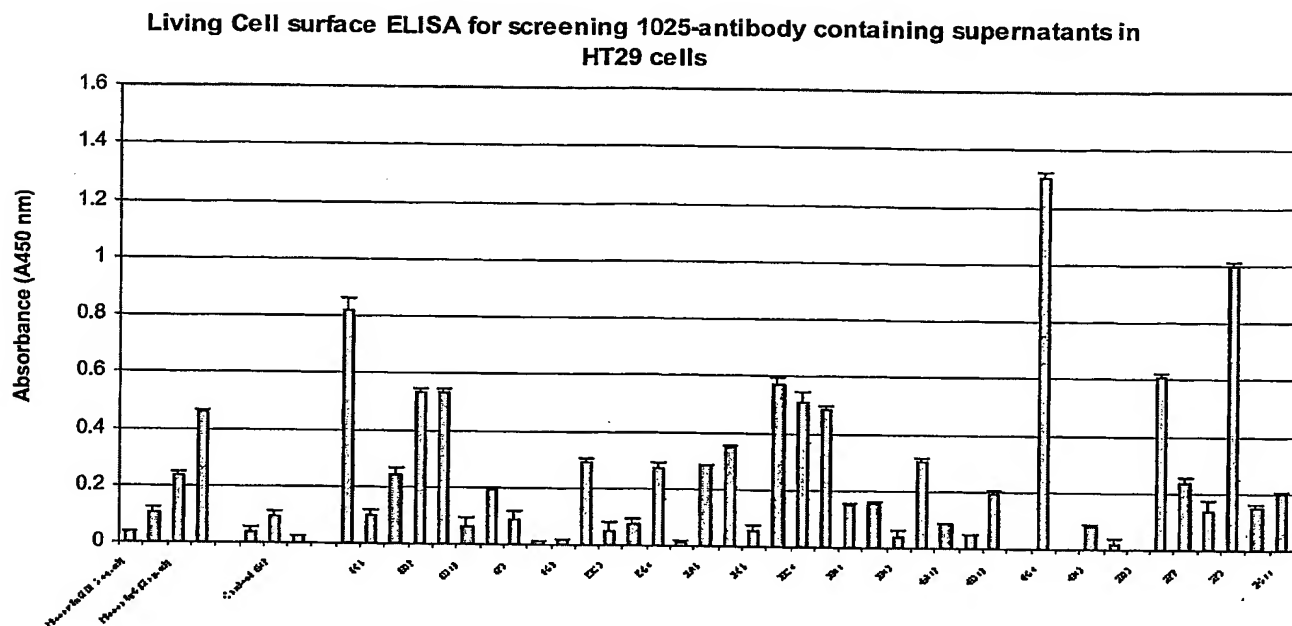
Figure 55. Screening of ICT1025 mAb for surface binding activities in breast tumor cell

The culture supernatants from 40 ICT1025 mAb secreting hybridoma clones were screened for the cell surface binding activities in MDA-MB-435 cells using a live cell surface staining ELISA assay. Mouse IgG at various concentration were used as non-specific controls. The clones with the highest cell surfsce binding activities (Absorbance value) were selected for mAb purification.

Figure 56. Screening of ICT1025 mAb for surface binding activities in colon tumor cells

The culture supernatants from 40 ICT1025 mAb secreting hybridoma clones were screened for the cell surface binding activities in HT29 cells using a live cell surface staining ELISA assay. Mouse IgG at various concentration were used as non-specific controls. Also, the supernatants from 3 GST mAb secreting hybridoma clones (2H2, 1H2, 3G3) were used as negative controls. The clones with the highest cell surfsce binding activities (Absorbance value) were selected for mAb purification.
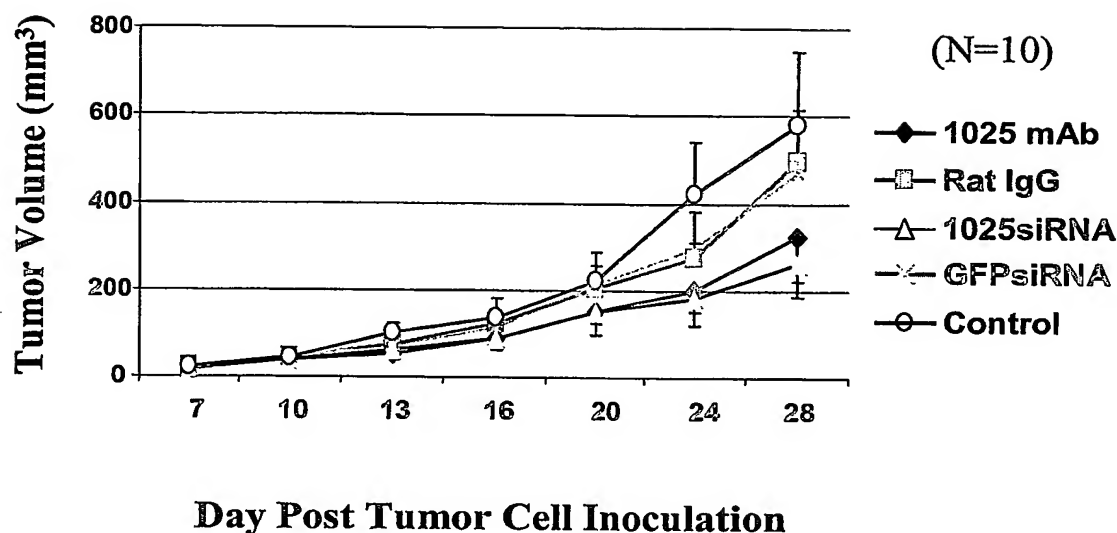
Day Post Tumor Cell Inoculation

Figure 57. Effect of inhibition of 1025 by antibody or siRNA on tumorigenesis and tumor growth. For antibody treatment, 5 million MDA-MB-435 cells were pre-incubated with 100 ug of 1025 mAb or Rat IgG in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site. For siRNA treatment, 5 million MDA-MB-435 cells in were transfected with 10 ug of 1025 siRNA or GFP siRNA using electroporation, then cells were incubated in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site. For control group, 5 million MDA-MB-435 cells were incubated in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site.